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Listing first 45 summaries
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Copyright (c) 1993 - 2003 Compugen Ltd.
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	21.	20,000	08/30	Chinn J,		L-MYERS S		92US-0816270.	91US-0642991.		92EP-0300429:								lasts; TG	rowth fac				(first entry)	updated)				lard; Prot		
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                                                      AAE05920;
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                                                                                                                                                                                                                                                                            CSSVKKYRPKYCGSCVDGRCCTPLQTRTVKMRFRCEDGEMFSKNVMMIQSCKCNYNCPHP
                                                                                                                                                                                                                                                                                                                                                     CGTGISTRVTNDNPECRLVKETRICEVRPCGQPVYSSLKKGKKCSKTKKSPEPVRFTYAG
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                                                                                                                                                                                                                                  interaction is used for the preparation of a medicament for the treatment of atherosclerosis, heart disease, tumour metastasis, fibrosis, tumour growth, disorders associated with inadequate angiogenesis; aberrant granulation tissue development; aberrant fibroblast growth and wounds. Polynucleotides of the invention
                                                                                                                                                                           Sequence
                                                                                                                                                                                                                       are useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cysteine-rich protein; Cyr61; extracellular matrix signalling mol fibroblast secreted protein; Fisp12; connective tissue growth fac CTGF; ECM; cell adhesion; cell migration; fibroblast cell prolife angiogenesis; wound healing; integrin receptor; atherosclerosis; heart disease; fibrosis; gene therapy; mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel human cysteine-rich protein 61 (Cyr61) fragment useful in methods for screening for modulators of cell adhesion, fibroblast cell proliferation, angiogenesis and cell migration
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06-OCT-2000;
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DB; AAD11220.
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                NEDCSKTQPCDHTKGLECNFGASSTALKGICRAQSEGRPCEYNSRIYQNGESFQPNCKHQ
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                                                                                                                   Conservative
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; 2000US-0204364.
; 2000US-0238705.
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Matches 379; Conser
                                                                                                                      The present invention describes human small CCN-like growth factor (SCGF). SCGF has vulnerary and osteopathic activities, and can be used in gene therapy. The SCGF polypeptides and polynucleotides can be used for treating muscle wasting diseases, and osteoporosis, and to stimulate wound healing and tissue regeneration, to promote angiogenesis and to stimulate proliferation of vascular smooth muscle and endothelial cell production. The present sequence represents a CNN family protein which is given in comparison with the human SCGF in the exemplification of the
                                                                         Sequence
                                                                                                                                                                                                                                                                                             Disclosure; Fig 2A-D;
                                                                                                                                                                                                                                                                                                                             WPI;
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gene therapy; muscle wasting disease; osteoporosis; wound healing;
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01-APR-1998;
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(ADAM/) ADAMS M D.
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 Score 2103; DB 23;
Pred. No. 3.7e-156;
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Query Match
Best Local Similarity
Matches 350; Conserv
                                                                                                       The present sequence represents a monocyte mature differentiation factor (MMDF) which maintains the life of macrophages for long per in liquid culture. MMDF can be used as an anti-cancer agent, an in activator and to treat infectious diseases.
                                                                       Sequence
                                                                                                                                                                                                     Claim
                                                                                                                                                                                                                                    A monocyte mature differentiation factor - tissue culture of macrophage(s)
                                                                                                                                                                                                                                                                                         WPI; 1997-497320/46
N-PSDB; AAT97142.
                                                                                                                                                                                                                                                                                                                                                                                   04-MAR-1996;
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                                                                                                                                                                                                 Page 12-13;
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                                                                       ΑĄ,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mature;
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                  92.2%;
                                                                                                                                                                                               22pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                differentiation ; tissue culture;
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 Score 1938; DB 18;
Pred. No. 2.9e-143;
9; Mismatches 18;
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; infectious disease.
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The present invention provides the protein and coding sequences of a number of human shear stress response proteins. These are useful in diagnosis, treatment and screening of vascular diseases caused by arteriosclerosis, including heart failure, post-PTCA restenosis and hypertension.
                                                                                                                                                                                                                                                                                      (KYOW )
(NOJI/)
                                                                                                                                          DNA sequences, proteins useful in diagnosis and
                                                                                                                                                                                                                                         Nojima
Kuga T,
                                                                                           Claim 60; Page 345-346; 678pp; Japanese.
                                                                                                                             arteriosclerosis
                                                                                                                                                                                                                                                                                                                                    01-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                 02-OCT - 2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human shear stress-response
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DB; AAH02896.
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yano S;
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                                                                                                                                                                                                                                                                              Human;
Cyr61;
                      Preventing uterine leiomyoma formation or inhibiting puterine leiomyoma in subject, comprises modulating or level of Cyr61 in leiomyoma tissue
 Disclosure;
                                                                       WPI; 2002-383245/41.
N-PSDB; ABK48899.
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92pp; English
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Pred. No. 2.9e-143;
9; Mismatches 18;
                                                                                                           Winneker
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local :
                                                                                                                                                                                         gene
                                                                                                                                                                                                                                          ischaemia; restenosis; tissue repair; wound healing; congenital defect; cardiovascular disease; atherosclerosis; heart failure; angina; trauma; burns; osteoporosis; periodontal disease; liver failure; tranquillizer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           of uterine leiomyoma or preventing uterine leiomyoma formation. The method comprises increasing the level of Cyr61 in leiomyoma tissue. The invention also describes compounds and compositions that stimulate induction of the Cyr61 gene and compounds that increase Cyr61 activity. The compositions and the method of the invention are useful for preventing uterine leiomyoma formation or inhibiting proliferation of uterine leiomyoma in a subject. The method is particularly useful for
                                                                                                                                        Homo
                                                                                                                                                                                                                                                                                                                                                                                  Human connective tissue growth factor-2 (CTGF-2).
                                                                                                                                                                                                                                                                                                                                       Human;
                                                                                                                                                                                                                                                                                                                                                                                                                                               07-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAE18107 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Note: The present sequence shown in Fig 6 is not shown in the correct sequence order in the figure. The start of the sequence is shown on page 8/10 of the figures and the rest of the sequence is shown on page 6/10 of the figures.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            uterine leiomyoma in a subject. The method is particularly useful for treating or preventing uterine leiomyoma formation, or inhibiting proliferation of uterine leiomyoma in a subject. The present sequence represents human Cyr61.
Region
                                                    Region
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                                                                                                                                                                                                                                                                                                                              angiogenesis;
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Location/Qualifiers 35..41 /note= "Immunogenic 47..51
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91.4%;
                 "Immunogenic epitope"
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                                                                                                                                                                                                                surgery; vasotropic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 1938; DB 23;
Pred. No. 2.9e-143;
9; Mismatches 18;
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The present invention relates to a method for stimulating angiogenesis in CC a mammal. The method comprises administering a polynucleotide encoding CC connective tissue growth factor-2 (CTGF-2) or an active fragment or its CC derivative. The method is useful for stimulating angiogenesis in a mammal CC preferably human having ischaemia or restenosis or is treated for limb CC revascularisation which is leg or arm. The invention is useful for cC inhibiting tumour growth, where angiogenesis is utilised for enhancing CC inhibiting tumour growth, where angiogenesis is utilised for enhancing CC fixation and stabilisation of tissue implants and enhancing wound CC fixation and stabilisation of tissue implants and enhancing wound CC fixating, hence is useful for treating cardiovascular disease e.g. CC atherosclerosis, reperfusion injury such as heart failure, angina, cC ischaemia, and is also used to differentiate, proliferate and attract CC cells leading to regeneration of tissues which is utilised to repair CC replace or protect tissue damaged by congenital defects, trauma (burns, closer, etc.), age, disease (e.g. osteoporosis, periodontal disease, the content of the process of the content of the process of the content of th
                     ulcer, etc), age, unsease (constant) plastic liver failure), surgery including cosmetic plastic sequence is human CTGF-2. CTGF-2 gene is useful in
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Query Match 92.2%; Best Local Similarity 91.4%; Matches 350; Conservative

Score 1938; DB 23; Pred. No. 2.9e-143; 9; Mismatches 18;

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The present invention describes a method for the prevention or inhibition of breast cancer cell proliferation. The method comprises administration of a compound that inhibits the interaction of a sex steroid receptor with a sex steroid response element of the Cyr6l (cysteine rich heparin-
                                                                                                                           Claim 6;
                                                                                                                                                              Regulation of Cyr61 expression and activity for preventing and inhibiting breast cancer comprises use of a Cyr61 neutralizing antibody, an anti-sense oligonucleotide and an antibody which
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CC binding protein) promoter. Cyr61 has cytostatic activity. An antibody (I) CC which neutralises Cyr61 can be used to prevent or inhibit breast cancer CC cell proliferation by blocking sex steroid induced and growth factor CC induced synthesis of Cyr61 DNA, where the growth factor is epidermal, CC heparin binding epidermal or basic fibroblastic growth factor. (I) can be CC used to diagnose or stage breast cancer where the level of Cyr61 in a CC positive/suspect breast cancer cell is compared to the level in a CC normal cell, an increase in the level of Cyr61 compared to the level in CC comman tissue indicates the presence of breast cancer. The level of Cyr61 being determined by exposing the tissues to (I), and an increase in the level of bound antibody by the suspect/positive cell as compared to the level of bound antibody by the suspect/positive cell as compared CC to the normal tissue indicates the presence of breast cancer. The present cancer represents the human Cyr61 protein, which is used in the CC exemplification of the present invention.
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                                                                    TYAGCLSVKKYRPKYCGSCVDGRCCTPQLTRTVKMRFRCEDGETFSKNVMMIQSCKCNYN
                                                                                       TYAGCSSVKKYRPKYCGSCVDGRCCTPLQTRTVKMRFRCEDGEMFSKNVMMIQSCKCNYN
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pred. No. 2.9e-143;
9; Mismatches 18;
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RESULT 9
AAB43987
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AAB43987 standard; Protein; 455

08-FEB-2001 (first entry)

aśsociated protein sequence SEQ ID NO:1432

Human; cancer associated gene; cancer antigen; detection; cancer; diagnosis; cytostatic; proliferative; vulnerary; immunomodulator; antidiabetic; antiasthmatic; antirheumatic; antiarthritic; antiviral; antiinflammatory; antithyroid; antiallergic; antibacterial; cardiant; dermatological; neuroprotective; thrombolytic; cagulant, nootropic; vasotropic; antipsoriatic; antiangiogenic; gene therapy; inflammation; immune disorder; haematopoietto cell disorder; autoimmune disorder; allergic reaction; graft versus host disease; organ rejection; neurological haemostatic; thrombolytic; disease; drug screening cardiovascular disorder;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cc in AAA4338 to AAA4439. The proteins can have activities based on the collection of activities and cells the genès are expressed in. Example of activities conclude: cytostatic; proliferative; vulnerary; immunomodulator; cantidiabetic; antiasthmatic; antirheumatic; antitarthritic; antidiabetic; antiasthmatic; antirheumatic; antitarthritic; concurrence and antiarthritic; concurrence and polypertotective; cardiant; thrombolytic; coagulant; concurrence; vasotropic; antipsoriatic and antiangiogenic. The concurrence and polypertides can be used for preventing, treating or ameliorating medical conditions and diagnosing pathological conditions. Complynucleotides, polypeptides, antibodies, againsts and antagonists from the present invention may be used to treat immune disorders by activating cor inhibiting the proliferation, differentiation or mobilisation of immune cells, to treat disorders of haematopoietic cells, autoimmune cells, altergic reactions, graft versus host disease and organ crejection, modulate haemostatic or thrombolytic activity, modulate cancers, cancers, cardiovascular disorders, neurological disease and crejection or viral infections. The peptides, nucleotides, antibodies, agonists and Anada4240 represent sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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Best Local :
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l for treating or
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Page 2116-2118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                455
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                                                                                                                                                                                                                                                                                                                                                                                                               Score 1938; DB 21;
Pred. No. 3.6e-143;
9; Mismatches 18;
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es based on the
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RESULT 10
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The invention discloses the isolated human polypeptides, and polynucleotides encoding them, that have been designated SECX and NOVX. The polypeptides can be used for treating, or delaying, the onset of an angiogenic-associated disorder or treating a pathological state in a subject, preferably a mammal. They can also be used in determining the presence of, or predisposition to, a disease associated with altered levels of the polypeptides and polynucleotides of any one of the 12 sequences (SEC1-12), for raising antibodies, for identifying an agent that binds to, or that modulates the expression or activity of the polypeptide, for treating or preventing a NOVX-associated disorder (NOVI-8) and as a pharmaceutical composition comprising the polypeptide, polypeptide or the antibody. The polypeptides and polynucleotides are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11-JAN-2001;
11-JAN-2001;
11-JAN-2001;
11-JAN-2001;
11-JAN-2001;
11-JAN-2001;
17-AUG-2001;
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Spytek KA,
                                                                                                                                                                                                                                                                                                                                                                                                 Human SECX/NOVX polypeptide useful for diagnosing, preventing or treating disorders associated with aberrant expression or activity SECX/NOVX nucleic acids and proteins e.g., diabetes
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Casman SJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     asthma; atherosclerosis; cardiomyopathy; angina pectoris; autoimmune disease; retinal disease; cirrhosis; diabetes; infectious disease; human immunodeficiency virus; HIV; cancer; hypertension; hypotension; multiple sclerosis; urinary retention; hypertension; multiple sclerosis; urinary retention; bosteoporosis; Crohn's disease; ulcer; neurological disorder; anxiety; becomes the property of the state of th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB;
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signal transduction pathway disorder; metabolic disorder;
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DB; ABS59522.
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E, Edinger
                                                                                                                                                                                                                                                                                                                                                  Page 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rastelli L, Herrmann JL, MacDougall Boldog F, Shimkets RA, Gorman L, C, Martin GB, Eisen A, Spaderna SK, Dipippo VA, Zerhusen BD, Peyman JA, Grosse WM, Alsobrook JP, Lepley DM,
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2001US-313170P.
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atory; angiogenic-associated disorder; diagnostic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local :
                                                                                                                                                                Cysteine rich protein 61; Cyr61; human; extracellular matrix signalling molecule; cell adhesion; cell migration; cell proliferation; angiogenesis; chondrogenes cell migration; cell proliferation; angiogenesis; chondrogenes
   18-SEP-1997
                                                                                                                                                                                                                                                                                                                                          Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW35730 standard;
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Pred. No. 1.2e-142;
0; Mismatches 19;
                                                                                                                                                                                                                                                                                                                                       (Cyr61).
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                                                                                                                                                                                                             chondrogenesis;
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N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        modulator of angiogenesis, chondrogenesis, oncogenesis, cell adhesion, cell migration, cell proliferation, expand a popula of undifferentiated haematopoietic stem cells in culture and screen for a mitogen (claimed). Ex vivo methods for using mammalian extracellular matrix signalling molecules to preparablood products are also provided.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAT94699). Cyr61 polypeptides can be expressed in transformed transfected host cells. Cyr61 can be used to modulate haematostasis, induce wound healing in a tissue, promote organ regeneration, improve tissue grafting or promote bone or proth implantation (claimed). It can also be used to screen for a capitation of continuous con
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This protein sequence comprises human cysteine rich protein (Cyr61), an extracellular matrix signalling molecule. Its a acid sequence was deduced from a human placental cDNA clone
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les 348; Conserv
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DB; AAT94699.
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e.g. haematostasis, induce
  CPHANEAAFPFYRLFNDIHKFRD
                                                                                                    TYAGCLSVKKYRPKYCGSCVDGRCCTPQLTRTVKMRFRCEDGETFSKNVMMIQSCKCNYN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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Pred. No. 1.5e
10; Mismatches
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381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein 61, Cyr61 - use wound healing, promote
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hes 19;
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(first entry)

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                                                                                                                                                               c protein (Fisp12) and connective tissue growth factor (CTGF) and connective tissue growth factor (CTGF) and conclete acid molecules encoding such proteins. The polypeptides c of the invention are members of cysteine-rich secreted protein c family. Human Cyr61 fragment is useful in methods for screening c modulators of cell adhesion, cell migration, fibroblast cell proliferation, angiogenesis, wound healing and Cyr61-integrin c receptor interaction. Modulator of Cyr61-integrin alphavbeta3 c interaction is used for the preparation of a medicament for the treatment of atherosclerosis, heart disease, tumour metastasis, fibroblast growth, disorders associated with inadequate angiogenesis; aberrant granulation tissue development; aberrant fibroblast growth and wounds. Polynucleotides of the invention are useful in gene therapy. The present sequence is human Cyr61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31-JAN-2000;
15-MAY-2000;
06-OCT-2000;
                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                 molecules involved in cellular response to growth factors. More particularly the invention is directed to cysteine-rich protein (Cyr61), and Cyr61-related proteins such as fibroblast secreted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           for screening i proliferation,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cysteine-rich protein; Cyr61; extracellular matrix signalling molecule; fibroblast secreted protein; Fisp12; connective tissue growth factor; CTGF; ECM; cell adhesion; cell migration; fibroblast cell proliferation; angiogenesis; wound healing; integrin receptor; atherosclerosis; tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                  The
                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel human cysteine:rich protein 61 (Cyr61) fragment useful in for screening for modulators of cell adhesion, fibroblast cell proliferation, angiogenesis and cell migration.
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                                                               Local Similarity
les 348; Conser
                                                                                                                                                                                                                                                                                                                                                                                                             invention relates to extracellular matrix (ECM)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2001-465561/50
                                                                                                                                                                                                                                                                                                                                                                                                                                           30; Page 171-172; 186pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cysteine-rich protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MUNIN CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAD11221.
MSSSTERTLAVAVTLLHLTRLALSTCPAACHCPLEAPKCAPGVGLVRDGCGCCKVCAKQL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Yeung C,
                                                                                                                         381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; 2000US-0495448.
; 2000US-0204364.
; 2000US-0238705.
                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2001WO-US03267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      fibrosis; gene therapy; human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= ".
282..381
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ocation/Qualifiers
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                                                                          91.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Domain IV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Domain III"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Cysteine free
                                                               10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (Cyr61).
                                                            Score 1929; DB 22;
Pred. No. 1.5e-142;
0; Mismatches 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           region"
                                                             Indels
                                                                                        Length
                                                                                                                                                                                                                                                                                                                                                                                                              signalling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         methods
                                                             Gaps
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RESULT 13
ABB09202
밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         δÃ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 В
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                    wound healing and tissue regeneration, to promote angiogenesis and to stimulate proliferation of vascular smooth muscle and endothelial cell production. The present sequence represents a CNN family protein which is given in comparison with the human SCGF in the exemplification of the
                                                                                                                                                                                                                                                        (HAST/)
                                                                                                                                                         Novel isolated polynucleotide sequence growth factor, useful for treating musc osteoporosis -
                                                                                                                                                                                                                                                                                                                                                                                                       Unidentified
                                                                   The present invention describes human small CCN-like growth fac (SCGF). SCGF has vulnerary and osteopathic activities, and can in gene therapy. The SCGF polypeptides and polynucleotides can for treating muscle wasting diseases, and osteoporosis, and to
                                                                                                                                  Disclosure;
                                                                                                                                                                                                                              Hastings GA,
                                                                                                                                                                                                                                                                                           06-JUN-1995;
01-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; small of
gene therapy;
                                                                                                                                                                                                          WPI; 2002-382150/41.
                                                                                                                                                                                                                                                                                                                               14-MAY-2001;
                                                                                                                                                                                                                                                                                                                                                         25-APR-2002
                                                                                                                                                                                                                                                                                                                                                                                US2002049304-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                  tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HCGF CNN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           08-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABB09202;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61
                                                                                                                                                                                                                                                                                                                                                                                                                                           small CCN-like growth factor;
nerapy; muscle wasting disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                 regeneration;
                                                                                                                                                                                                                                                        HASTINGS
ADAMS M D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 family protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CTCIDGAVGCIPLCPQELSLPNLGCPNPRLVKVSGQCCEEWVCDEDSIKDSLDDQDDL--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NEDCSKTQPCDHTKGLECNFGASSTALKGICRAQSEGRPCEYNSRIYQNGESFQPNCKHQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CPHANEAAFPFYRLFNDIHKFRD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CPHPNEASFRLYSLFNDIHKFRD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYAGCSSVKKYRPKYCGSCVDGRCCTPLQTRTVKMRFRCEDGEMFSKNVMMIQSCKCNYN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CSKSCGTGISTRVTNDNPECRLVKETRICEVRPCGQPVYSSLKKGKKCSKTKKSPEPVRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KELGFDASEVELTRNNELTAVGKGRSLKRLPVFGMEPRILYNPL--QGQKCIVQTTSWSQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                --LGLDASEVELTRNNELIAIGKGSSLKRLPVFGTEPRVLFNPLHAHGQKCIVQTTSWSQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CTCIDGAVGCIPLCPQELSLPNLGCPNPRLVKVTGQCCEEWVCDEDSIKDPMEDQDGLLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYAGCLSVKKYRPKYCGSCVDGRCCTPQLTRTVKMRFRCEDGETFSKNVMMIQSCKCNYN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CSKTCGTGISTRVTNDNPECRLVKETRICEVRPCGQPVYSSLKKGKKCSKTKKSPEPVRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NEDCSKTQPCDHTKGLECNFGASSTALKGICRAQSEGRPCEYNSRIYQNGESFQPNCQHQ
                                                                                                                                 Fig
                                                                                                                                                                                                                                                                                                                                 2001US-0853625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first
                                                                                                                                                                                                                                 Adams
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98US-0053587
                                                                                                                                                                                                                                                        S G A.
                                                                                                                                  2A-D;
                                                                                                                                                                                                                                 ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                  angiogenesis.
                                                                                                                                  33pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          374
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                                                                                                                                                                     muscle
                                                                                                                                                                                                                                                                                                                                                                                                                                            SCGF; vulnerary; osteopathic;
; osteoporosis; wound healing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IJ
                                                                                                                                                                     encoding a
cle wasting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NO:12
                                                                                                                                                                   human small CCN-like disease, and
                                                                                n factor
can be used
can be used
                                                                      stimulate
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RESULT 14
AAR90919
ID AAR90
XX AAR90
AC AAR90
XZ 25-MA
DT 25-MA
DT 25-MA
DT 25-MA
CTGF-
KW CTGF-
KW CTGF-
KW Insul
XX Insul
XX Homo
XX Homo
XX WO96C
XX WO96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                    N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTGF-2; connective tissue growth factor-2; secreted protein; cartilagenous growth; skeletal; embryo; cell growth; morphogenesis; insulin-like growth factor; fibroblast growth factor; Cry61.
                                           WPI; 1996-097626/10
                                                                                       Adams
                                                                                                                                                                         12-JUL-1994;
                                                                                                                                                                                                                                                                                                                                                                               Protein
                                                                                                                                (HUMA-)
                                                                                                                                                                                                                     12-JUL-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25-MAR-2003
25-JUN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAR90919;
                                                                                                                                                                                                                                                              25-JAN-1996.
                                                                                                                                                                                                                                                                                                            WO9601896-A1
                                                                                                                                                                                                                                                                                                                                                                                                                      Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Connective tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAR90919 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
les 332; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61
                      AAT12653
                                                                                                                              HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FTYAGCSSVKKYRPKYCGSCVDGRCCTPLQTRTVKMRFRCEDGEMFSKNVMMIQSCKCNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTCIGWRRGACIPLCPQELSLPNLGCPNPRLVKVTGQCCEEWVCDEDSIKDPMEDQDGLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CTCIDGAVG-CIPLCPQELSLPNLGCPNPRLVKVSGQCCEEWVCDEDSIKDSLDDQDDL- 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NEDCSKTQPCDHTKGLECNFGASSTALKGICRAQSEGRPCEYNSRIYQNGESFQPNCKHQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCPHPNEASFRLYSLF 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MSSRIVRELALVVTLLHLTRVGLSTCPADCHCPLEAPKCAPGVGLVRDGCGCCKVCAKQL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (updated)
(first entry)
                                                                                    Η;
                                                                                                                                GENOME
                                                                                                                                                                         94WO-US07736
                                                                                                                                                                                                                     94WO-US07736
                                                                                                                                                                                                                                                                                                                                                                        /label= signal_peptide 25..375
                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
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                                                                                                                                SCI INC
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88.3%; Pred. No. 5.1
Live 10; Mismatches
                                                                                                                                                                                                                                                                                                                                                      mature_protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         factor-2
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nes 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length
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RESULT 15
AAY31620
ID AAY31
XX AAY31
XX AAY31
XX AAY31
XX O2-NC
XX Human
XX Conne
XW Skin
XX Skin
XX Homo
XX Homo
XX Homo
XX Key
FT Pepti

Human 02-NOV-1999

CTGF-2

(first entry)

AAY31620

standard;

Protein;

375

A

Homo sapiens

Peptide

/label= Signal_peptide Location/Qualifiers Connective tissue growth factor-2; CTGF-2; wound healing; bone disorder; skin disorder; acne; burn; UV damage; stabilisation; tissue implant.

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Matches 332;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Connective tissue growth factor-2 (CTGF-2) is encoded by a cDNA (AAT12653) isolated from a human foetal lung cDNA library. The GTGF polypeptides are structurally and functionally related to a family of growth factors which include IGF (Insulin-like growth factor), PDGF (platelet-derived growth factor), and FGF (fibroblast growth factor). CTGF-2 exhibits 89 percent identity and 93 percent similarity to CTy61 is a growth factor-inducible immediate early gene initially identified in serum-stimulated mouse fibroblasts. It encodes a member of an emerging family of secreted proteins which are also a group of cysteine-rich proteins. This group of GFs are important for normal growth, differentiation, morphogenesis of the cartilaginous skeleton of an embryo and cell growth. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1;
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                                                            QCSKSCGTGISTRVTNDNPECRLVKETRICEVRPCGQPVYSSLKKGKKCSKTKKSPEPVR
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 NCPHANEAAFPFYRLF
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                               NCPHPNEASFRLYSLF 371
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Matches 332; Conserv
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12-JUL-1994;
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                                                                                                                                                                                                                                                                                                             86.5%; Score 1819.5; DB 20; Length 375;
88.3%; Pred. No. 5.1e-134;
Live 10; Mismatches 27; Indels 7;
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Search completed: August Job time: 40.8974 secs
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                                               NCPHANEAAFPFYRLF 374
                                                                 NCPHPNEASFRLYSLF 371
                                                                                            QCSKTCGTGISTRVTNDNFECRLVKETRICEVRPCGQPVYSSLKKGKKCSKTKKSPEPVR
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Title: Perfect score:

Run on: 8

protein -

Minimum DB Maximum DB Minimum

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Searched:

Scoring table:

Sequence 2, Appli Sequence 16, Appl Sequence 17, Appl Sequence 37, Appl Sequence 38, Appli Sequence 6, Appli Sequence 4, Appli Sequence 8, Appli Sequence 7, Appli Sequence 7, Appli Sequence 21, Appli Sequence 22, Appli Sequence 21, Appli Sequence 21, Appli Sequence 21, Appli Sequence 21, Appli Sequence 31, Appli Sequence 31, Appli Sequence 31, Appli Sequence 31, Appli

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Post-processing: Minimum Match 0%
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length: 2000000000
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Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
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/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/BCTUS_COMB.pep:*
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US-08-468-47B-12
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US-09-142-569-6
US-08-167-628-2
US-08-167-628-2
US-08-18-15-17-2
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US-09-056-704-2
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13, Appl.
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15, Appl.
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US-08-468-847B-11
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Matches 379
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                                                                                                                                                                                                                             TELEFAX: 201-994-1744 INFORMATION FOR SEQ ID NO: 11:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:

NAME: MULLINS, J.G.

REGISTRATION NUMBER: 33,073

REFERENCE/DOCKET NUMBER: 3258

TELECOMMUNICATION INFORMATION:

TELEPHONE: 201-994-1700
                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: U. FILING DATE: 6 June 1 CLASSIFICATION: 435
PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
                                                                                                                              STRANDEDNESS:
TOPOLOGY: LINEAR
MOLECULE TYPE: PRO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Hastings, Gregorithm of INVENTION: Human NUMBER OF SEQUENCES: 20
                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                               LENGTH:
TYPE: A
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CITY: ROSELAND
STATE: NEW JERSEY
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US-08-468-847B-16
US-08-468-847B-16
US-08-68-847B-17
US-09-253-316-25
US-09-182-145-6
US-09-182-145-6
US-09-182-145-8
US-09-182-145-8
US-09-182-145-21
US-09-182-145-21
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US-09-182-145-37
US-09-182-145-37
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                                                 $core 2103; DB 1;
Pred. No. 4.2e-170;
; Mismatches 0;
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& OLSTEIN
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-Like Growth Factor
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Result No.

Match

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              equence 2, Application US/09142569 atent No. 6413735 GENERAL INFORMATION:
                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION: INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 2:
/ Match
Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/09/142,569
FILING DATE: 02-Apr-1999
CLASSIFICATION: CURKOWNS
ATTORNEY/AGENT INFORMATION:
                                                                      SEQUENCE DESCRIPTION:
                                                                                                                                FEATURE:
                                                                                                                                               MOLECULE TYPE: protein
                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 379 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Lau, Lester F. TITLE OF INVENTION: Extracellular Matrix Signalling Molecules NUMBER OF SEQUENCES: 17
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                                                                      NAME/KEY: misc_feature
OTHER INFORMATION: "Mouse
ENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTCIDGAVGCIPLCPQELSLPNLGCPNPRLVKVSGQCCEEWVCDEDSIKDSLDDQDDLLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Chicago
STATE: Illinois
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                                                                                                                                                                  TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                   NAME: Clough, David W. REGISTRATION NUMBER: 36,107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: United States of America ZIP: 60606-6402
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                                                                                                                                                                                        TYPE: amino acid
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Pred.
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 2103; DB 4;
No. 4.2e-170;
                                                                          Cyr61 amino 2:
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                                                                                             acid
                 Length 379;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     #1.30
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Query Match
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                                                                                                                                                                  INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                    COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Ver:
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/09/348,815
FILING DATE: 08-011-199
CLASSIFICATION: <Unknown>
ATTORNEY/ACENT INFORMATION:
NAME: JONATHAN L. KLEIN
REGISTRATION UMBER: 41,119
REFERENCE/DOCKET NUMBER: PF126P1D1
                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-309-8504
TELEFAX: 301-309-8439
                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                     MOLECULE TYPE: protein SEQUENCE DESCRIPTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: CONNECTIVE TISSUE GROWTH FACTOR-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            301
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                                                                                          TOPOLOGY: linear
                                                                                                               TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: ROCKVILLE STATE: MD
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                                                                                                                              LENGTH: 381 amino acids
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92.2%;
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Length 381;
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                                                                                                                                     TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
                                    FEATURE:
                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION:
                                                   MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: I
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KELGFDASEVELTRNNELIAVGKGSSLKRLPVFGMEPRILYNPL--QGQKCIVQTTSWSQ
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                                                                                    LENGTH: 381 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/09/142,569
FILING DATE: 02-Apr-1999
CLASSIFICATION: <Unknown>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CPHPNEASFRLYSLFNDIHKFRD 379
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 NAME/KEY: misc_feature
OTHER INFORMATION: "H
                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: United States of America ZIP: 60606-6402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Chicago
                 NAME/KEY:
                                                                                                                                                                   TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Marshall,
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SYSTEM: PC-DOS/MS-DOS
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rower, 233
                                                                                                                                                                                                                                        36,107
"Human Cyr61 amino acid sequence"
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.ches 18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-468-847B-12
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Patent No. 5780263
GENERAL INFORMATI
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Best Local Similarity
Matches 348; Conser
                 TELEFAX: 201-99
INFORMATION FOR SEQ
                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INC
COMPUTER: IBM PS/2
                                                 REFERENCE/DOCKET NUMBER: 32
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: HUNUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                   CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                    OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
                                                                                                                                  ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
                                                                                                  NAME: MULLINS, J.G. REGISTRATION NUMBER:
                                                                                                                                                                                                                    APPLICATION NUMBER: FILING DATE: 6 June
                                                                                                                                                     FILING DATE:
                                                                                                                                                                     APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                        CITY: ROSELAND
STATE: NEW JERSEY
                                                                                                                                                                                                                                                                                                                                                                                                                          STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: CARELLA, BYRNE,
ADDRESSEE: CECCHI, STEWART
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                               201-994-1744
                                                                                                                                                                                                                                                                                                                                                                        USA
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90.9%;
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Pred. No. 2.
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US-08-459-101A-2
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Matches
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TOPOLOGY: LII
MOLECULE TYPE:
REFERENCE/DOCKET NUMBER: 35:134
TELECOMMUNICATION INFORMATION
                                                                                  APPLICATION NUMBER: PCT/
FILING DATE: 12 JUL 94
ATTORNEY/AGENT INFORMATION:
                                                                                                                                 APPLICATION NUMBER: US/08/459,101A FILING DATE: June 2, 1995 CLASSIFICATION: 536 PRIOR APPLICATION DATA:
                                                                                                                                                                                                              SOFTWARE: WORD PERFECT CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM: MEDIUM TYPE: 3.5 INC
                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: CO
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                                                                                                                                            COMPUTER: IBM PS/
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                               STREET:
                                                NAME: FERRARO, GREGORY D. REGISTRATION NUMBER: 36,1
                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: CARELLA, BYRNE, BAIN, GIL
ADDRESSEE: CECCHI, STEWART & OLSTEIN
STREET: 6 BECKER FARM ROAD
                                                                                                                                                                                                                                                                                   MEDIUM TYPE:
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NEW JERSEY
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AMINO ACID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FTYAGCSSVKKYRPKYCGSCVDGRCCTPLQTRTVKMRFRCEDGEMFSKNVMMIQSCKCNY 355
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ---LGLDASEVELTRNNELIAIGKGSSLKRLPVFGTEPRVLFNPLHAHGQKCIVQTTSWS 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTCIGWRRGACIPLCPQELSLPNLGCPNPRLVKVTGQCCEEWVCDEDSIKDPMEDQDGLL
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                                                                                                                                                                                                                                                                                                                                         USA
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                                                                                                                                                                                                                             SYSTEM: MS-DOS
WORD PERFECT 5.1
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88.3%; Pred. No. 3.9e-146;
Live 10; Mismatches 27;
                                                                                                                       PCT/US94/07736
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                               325800-317
                                                                                                                                                                                                                                                                                                                                                                                                                               GILFILLAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                Patent No. 5780263 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 13,
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Best Local :
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TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 375 AMINO ACIDS
                                                                                                                                     COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
                                                               CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
                                                                                                                                                                                                                                                            STREET: 0 L.
STREET: NOSELAND
CITY: ROSELAND
CTATE: NEW JERSEY
                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: HUNUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                APPLICATION NUMBER:
                                                                                                   APPLICATION NUMBER: FILING DATE: 6 June
                                                                                                                                                                                                                                                 COUNTRY: UZIP: 07068
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NEDCSKTQPCDHTKGLECNFGASSTALKGICRAQSEGRPCEYNSRIYQNGESFQPNCKHQ
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E: CECCHI, STEWART
6 BECKER FARM ROAD
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              INFORMATION
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Pred. No. 1.5e-145;
0; Mismatches 28;
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; MOLECULE TYPE:
US-08-468-847B-13
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Matches
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APPLICANT: Japan Tobacco,
 Query Match
Best Local Similarity
                                                                                           SEQ ID NO 2
                                                                                                                                                                        TITLE OF INVENTION: Monoclonal Antibody Against Connective Tissue Growth Factor TITLE OF INVENTION: and Medicinal Uses Thereof FILE REFERENCE: J1-009PCT CURRENT APPLICATION NUMBER: US/09/582,337 CURRENT FILING DATE: 2000-06-23 PRIOR APPLICATION.
                                                                                                                                                                                                                                                                           Sequence 2, Application US/09582337 Patent No. 6562618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                     NUMBER OF SEQ ID NOS: 27 SOFTWARE: Patentin Ver.
                                                                                                                              PRIOR APPLICATION NUMBER: JP P1998-356183 PRIOR FILING DATE: 1998-12-15
                                                                                                                                                        PRIOR APPLICATION NUMBER: JP P1997-367699 PRIOR FILING DATE: 1997-12-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 13: SEQUENCE CHARACTERISTICS:
                                                                             LENGTH: 347
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REFERENCE/FOCKET NUMBER: 32!
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
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TELEFAX: 201-994-1744
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Pred. No. 1.7e-131;
2; Mismatches 36;
Score 958; DB 4;
Pred. No. 2.6e-73;
            Length
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                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 178; Conserv
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PRIOR FILING DATE: 1999-04-14
PRIOR APPLICATION NUMBER: US 09/187,478
PRIOR FILING DATE: 1998-11-06
NUMBER OF SEQ ID NOS: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: SVERDRUP, Fran APPLICANT: CARMICHAEL, David APPLICANT: CARMICHAEL, David TITLE OF INVENTION: CONNECTIVE TISSUE GROWTH FACTOR (CTGF) AND METHODS FILE REFERENCE: FIBRO1100-1 CURRENT APPLICATION NUMBER: US/09/292,036 CURRENT FILING DATE: 1999-04-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: FIBROGEN, INC
APPLICANT: SCHMIDT, Brian
                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn version
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                   KHQCTCIDGAVGCIPLCPQELSLPNLGCPNPRLVKVSGQCCEEWVCDEDSIKDSLDDQDD 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QLNEDCSKTQPCDHTKGLECNFGASSTALKGICRAQSEGRPCEYNSRIYQNGESFQPNCK 118
                                                                                                KQLNEDCSKTQPCDHTKGLECNFGASSTALKGICRAQSEGRPCEYNSRIYQNGESFQPNC 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HQCTCIDGAVGCIPLCPQELSLPNLGCPNPRLVKVSGQCCEEWVCDEDSIKDSLDDQDDL 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MLASVAGPVSLALVLLLCTRPATGQDCSAQCQCAREAAPRCPAGVSLVLDGCGCCRVCAK
KYQCTCLDGAVGCVPLCSMDVRLPSPDCPFPRRVKLPGKCCEEWVCDEP-
                                                                         KQLGELCTERDPCDPHKGLFCDFGSPANRKIGVCTAK-DGAPCVFGGSVYRSGESFQSSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PHPNEASFRLY -- SLFNDI 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QLGELCTERDPCDPHKGLFCDFGSPANRKIGVCPAK-DGAPCVFGGSVYRSGESFQSSCK 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----KDRTVVGPALAAYRLEDTFGPDPTMM-----RANCLVQTTEWSAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ALLEN, Margaret
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                            45.5%;
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                                                                                                                                                                                                                                          Score 957.5; DB 4
Pred. No. 2.9e-73;
                                                                                                                                                                                                                             Mismatches
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                                                                                                                                                                                                                                                                DB 4;
                                                                                                                                                                                                                             103;
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US-08-468-847B-15
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                                                                                                                                                     Matches
                                                                                                                                                                                    Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 15,
                                                                                                                                                                                                                                                                                                                 TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 435
PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM: MEDIUM TYPE: 3.5 INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Hastings,
TITLE OF INVENTION: I
                                                                                                                                                                                                                                      MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                   NAME: MULLINS, J.G.
REGISTRATION NUMBER: 33,073
REFERENCE/DOCKET NUMBER: 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 6 June 1995 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: ROSELAND
STATE: NEW JERSEY
                                                                                                                                                                     Local
                                                                                                                                                                                                                                                    TOPOLOGY:
                                                                                                                                                                                                                                                                    STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET:
                                                                                                                                                                                                                                                                                                    LENGTH:
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                                                                                                                                                     177;
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5780263
                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                   AMINO ACID
                                              KQLNEDCSKTQPCDHTKGLECNFGASSTALKGICRAQSEGRPCEYNSRIYQNGESFQPNC 117
                                                                                MLASVAGPISLALVLLALCTRPATGQDCSAQCQCAAEAAPHCPAGVSLVLDGCGCCRVCA
                                                                                                       MSSSTFRTLAVAVTLLHL-TRLAL-STCPAACHCPLE-APKCAPGVGLVRDGCGCCKVCA 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ELSGCTSVKTYRAKFCGVCTDGRCCTPHRTTTLPVEFKCPDGEIMKKNMMFIKTCACHYN 327
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                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                      LINEAR
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CECCHI, STEWART
                                                                                                                                                                                                                                                                                                                                                                      201-994-1700
                                                                                                                                                                                                                                     PROTEIN
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                                                                                                                                                    61,
                                                                                                                                                                 Score 953.5; DB 1; Pred. No. 6.3e-73;
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                                                                                                                                                    Mismatches
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US-09-142-569-6
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                                                               Best Local Similarity Matches 177; Conserv
                                                                                                Query Match
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Patent No. 6413735
                                                                                                                                                                                                                                                                                                                  TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                               NAME/KEY: misc_feature
OTHER INFORMATION: "Fisp12 amino
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                               NAME: Clough, David W.
REGISTRATION NUMBER: 36,1
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                    FEATURE:
                                                                                                                                                                                                                   MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Extracellular Matrix Signalling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Lau,
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                             MSSSTFRTLAVAVTLLHL-TRLAL-STCPAACHCPLE-APKCAPGVGLVRDGCGCCKVCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYAGCSSVKKYRPKYCGSCVDGRCCTPLQTRTVKMRFRCEDGEMFSKNVMMIQSCKCNYN 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CSKTCGMGISTRVTNDNTFCRLEKQSRLCMVRPCEADLEENIKKGKKCIRTPKIAKPVKF
MLASYAGPISLALVLLALCTRPATGQDCSAQCQCAAEAAPHCPAGVSLVLDGCGCCRVCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KHQCTCIDGAYGCIPLCPQELSLPNLGCPNPRLYKYSGQCCEEWYCDEDSIKDSLDDQDD 177
                                                                                                                                                                                                                                   STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                                                                    TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/09/142,569 FILING DATE: 02-Apr-1999 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CPHPNEASFRLY -- SLFNDI 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ELSGCTSVKTYRAKFCGVCTDGRCCTPHRTTTLPVEFKCPDGEIMKKNMMFIKTCACHYN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LLGLDASEVELTRNNELIAIGKGSSLKRL-PVFGTEPRVLFNPLHAHGQKCIVQTTSWSQ 236
                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KYQCTCLDGAVGCVPLCSMDVRLPSPDCPFPRRVKLPGKCCKEWVCDEP--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 60606-6402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: United
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET:
                                                                                                                                                                                                                                                                                     LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Marshall,
                                                                 Conservative
                                                                                                                                                                                                                                                                                     348 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6300 Sears Tower,
                                                                                45.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   States of America
                                                                 61; Mismatches 103;
                                                                                Score 953.5; DB 4
Pred. No. 6.3e-73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   O'Toole, o'Tower, 233
                                                                                                                                                                                                                                                                                                                                                                                                                      36,107
                                                                                                                                                                                                                                                                                                                                                                                                     28758/33766
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gerstein, Murray & South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Version #1.30
                                                                                                DB 4;
                                                                                                                                                                   acid
                                                                                                                                                                 sequence"
                                                                 Indels
                                                                                                Length 348;
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В Qy

39;

Gaps

60 57 Qy

170

351 263 291 203 231 115

56

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; MOLECULE TYPE: US-08-167-628-2
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US-08-167-628-2
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Patent No.
                                                  Query Match
                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                  TELEBAX: 619-455-5110
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 349 amino acids
                                                                                                                                                                                                                  NAME: Wetherell, Jr. Ph.D., John W. REGISTRATION NUMBER: 31,678
REFERENCE/DOCKET NUMBER: PD-1294
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-455-5100
                                                                                                                                                                                                                                                                                                   FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Rel
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Grotendorst, Gary R.
APPLICANT: Bradham Jr., Douglas M.,
TITLE OF INVENTION: CONNECTIVE TISSUE GROWTH FACTOR
NUMBER OF SEQUENCES: 2
                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                  Local Similarity
                                                                                                                    TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                   NAME: Wetherell, Jr. REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KQLNEDCSKTQPCDHTKGLECNFGASSTALKGICRAQSEGRPCEYNSRIYQNGESFQPNC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Jolla
                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                        IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                 protein
                                  45.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Release #1.0, Version
                                                                                                                                                                                                                                                                                                                                         US/07/752,427
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                                                                                                                                                                                                                                                                                                                                                                                                         US/08/167,628
                   64;
            Score 950; DB 1; Pred. No. 1.2e-72; "" matches 97;
                                               Length 349;
                 Indels
                 48;
                 Gaps
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US-08-386-680-2
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TOPOLOGY: 1:
MOLECULE TYPE:
-08-386-680-2
                                                                                                                           ATTORNEY AGENT INFORMATION:

NAME: Wetherell, Jr. Ph.D., J.

REGISTRATION NUMBER: 91,678

REFERENCE/DOCKET NUMBER: PD-1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 619-455-5100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                 TELEFAX: 619-455-5110
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Bradham Jr., TITLE OF INVENTION: CON NUMBER OF SEQUENCES: 2
                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
ZIP: 920
                                                                                                                                                                                                                                                  FILING DATE:
APPLICATION NUMBER: US/07/752,427
                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/0:
FILING DATE: 10-FEB-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET:
                                                                LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACHYNCPGDNDIFESLYYRKMYGDM 348
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                                                                349 amino acids
                                                                                                                    619-455-5110
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                                  linear
                                                                                                                                                                                                                                                                                                                                                                                                                                       Floppy disk
                 protein
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                  INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 349 amino acid
                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Grotendorst, Gary R.
APPLICANT: Bradham Jr., Douglas M.,
TITLE OF INVENTION: CONNECTIVE TISSUE GROWTH FACTOR
                                                                 TELECOMMUNICATION INFORMATION: TELEPHONE: 619-455-5100
                                                                                                                                                                   PRIOR APPLICATION DATA:

APPLICATION NUMBER: US C
FILING DATE: 30-AUG-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                NAME: Wetherell, Jr. Ph.D., John W. REGISTRATION NUMBER: 31,678
REFERENCE/DOCKET NUMBER: PD-1294
                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                                                                                                                                                                   CLASSIFICATION:
                                                                                                                                                                                                                               APPLICATION NUMBER: US/0 FILING DATE: 02-JUN-1995
                                                                                                                                                                                                                                                                                     SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CRVCAKQLGELCTERDPCDPHKGLFCDFGSPANRKIGVCTAK-DGAPCIFGGTVYRSGES 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CKVCAKQLNEDCSKTQPCDHTKGLECNFGASSTALKGICRAQSEGRPCEYNSRIYQNGES 112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MTAASMGPVRVAFVVL----LALCSRPAVGQNCSGPCRCPDEPAPRCPAGVSLVLDGCGC
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 349 amino acids
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                                                                                                                                                                                                                                                                                                 IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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45.7%;
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Pred. No. 1.2e-72;
Pred. Mismatches 97;
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Best Local
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                             KCNYNCPHPNEASFRLY -- SLFNDI 374
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Pred. No. 1.2e-72;
4; Mismatches 97;
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RESULT 15 US-08-712-302-2 Sequence 2, Application Patent No. 5783187 GENERAL INFORMATION: COMPOTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA: COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk ATTORNEY/AGENT INFORMATION: NAME: Wetherell, Jr. Ph. PRIOR APPLICATION DATA: CORRESPONDENCE ADDRESS TITLE OF INVENTION: APPLICANT: APPLICANT: ADDKL.
STREET:
La Jo.
TTY: CA NUMBER OF SEQUENCES: REGISTRATION NUMBER: 31,678 APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: US 0 FILING DATE: 10-FEB-1995 CLASSIFICATION: APPLICATION NUMBER: US/08 FILING DATE: 11-SEP-1996 FILING DATE: FILING DATE: COUNTRY: 92037 E: Spensley Horn Jubas & Lubitz 4225 Executive Square, Suite 1400 Bradham Jr., Douglas M., VENTION: CONNECTIVE TISSUE GROWTH US Jolla Grotendorst, Gary R. NUMBER: us/08712302 US/08/712,302 US 08/386,680 US/07/752,427 US/08/167,628 PD-1294 FACTOR

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: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 619-455-5110
: TELEFAX: 619-455-5110
: INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 349 amino acids
: TYPE: amino acids
: TYPE: mino acids
: TYPE: mino acids
: TYPE: protein
US-08-712-302-2
Search completed: August 5, 2003, 14:08:01 Job time: 14.9632 secs
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                                                                                                                         232 TSWSQCSKSCGTGISTRYTNDNPECRLYKETRICEVRPCGQPYYSSLKKGKKCSKTKKSP 291
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                                                                                          352 KCNYNCPHPNEASFRLY--SLFNDI 374
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Result
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Maximum DB
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Listing first 45 summaries
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4 US-10-101-040-3
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4 US-10-053-753-2
1 US-09-901-910-2
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5 US-10-294-796-2
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11, Applice 2, Applice 2, Applice 2, Applice 4, Applice 4, Applice 4, Applice 4, Applice 17, Applice 7, Applice 8, Applice 6, Applice 6, Applice 6, Applice 8, Applice 6, Applic
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621	622	622	622	758.5	58	772	772	772	772	773	773	773	773	773	839.5	839.5	861	919	937	941.5	944	944	950	950	950	950	950	950	950	
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US-10-112-267-32	US-10-112-267-37	US-10-011-859-2	- 1	US-10-112-267-12	4			US-10-112-267-21	US-10-112-267-5	US-10-112-267-8	US-10-112-267-4	US-10-001-054-50			US-10-011-859-25		9-853-6	0-245	-10-245-977-	US-09-853-625B-14	-10-101-	-10-080-173-	-10-245-	US-10-205-823-78	-10-171-311-	US-10-060-036-173	Ψ	-10-011-	US-10-101-040-4	
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ALIGNMENTS

US-09-853-625B-11
US-09-853-625B-11
Sequence 11, Application US/09853625B
Patent NO. US20020049304A1
Patent NO. US20020049304A1
PAPPLICANT: Hastings, Gregg A. and Adams, Mark D. TITLE OF INVENTION: Human CCN-Like Growth Factor NUMBER OF SEQUENCES: 20
CCRRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILIAN, STREET: 6 BECKER FARM ROAD CITY: ROSELAND STATE: NEW JERSEY
COUNTRY: USA
ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER WADDABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER WORD PERFECT 5.1
CURRENT APPLICATION NUMBER: US/09/853,625B
FILING DATE: 14 May-2001
CLASSIFICATION STATE: 14 May-2001
CLASSIFICATION STATE: 14 May-2001
CLASSIFICATION NUMBER: 09/053,587
PRIOR APPLICATION NUMBER: 09/053,587
REPERENCE/DOCKET NUMBER: 33,073
REFERENCE/DOCKET NUMBER: 325800-442
TELEPHONE: 201-994-1700
TELEPAX: 201-994-1700
TELEPAX: 201-994-1700
TELEPAX: 201-994-1700
LENGTH: 379 AMINO ACIDS

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Gaps

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RESULT 2
US-10-053-753-2
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INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                      COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION NUMBER: US/10/053,753

FILING DATE: 22-Jan-2002

CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:

NAME: Clough, David W.

REGISTRATION NUMBER: 36,107

REGISTRATION NUMBER: 36,107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local
                                                                      TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Lau, Lester F.
TITLE OF INVENTION: Extracellular Matrix Signalling Molecules NUMBER OF SEQUENCES: 17
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STRANDEDNESS: «Unknown»
TOPOLOGY: LINEAR
MOLECULE TYPE: PROTEIN
SEQUENCE DESCRIPTION: SEQ ID NO:
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379; Conserv
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               TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
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                                                                                                                                                                                                                                                                                                                                                                              CITY: Chicago
STATE: Illinois
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                                                                                    REFERENCE/DOCKET NUMBER: 28758/33766
                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Marshall, O'Too
STREET: 6300 Sears Tower,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LDASEVELTRNNELIAIGKGSSLKRLPVFGTEPRVLFNPLHAHGQKCIVQTTSWSQCSKS
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NO:
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lower, 233
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Pred. No. 3.2e-167;
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                                                 SOFTWARE: Patentin
SEQ ID NO 2
LENGTH: 381
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                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/901,910 CURRENT FILING DATE: 2001-07-11 PRIOR APPLICATION NUMBER: 09/348,815 PRIOR FILING DATE: 1999-07-08, PRIOR PLICATION NUMBER: 08/459,101 PRIOR FILING DATE: 1995-06-02
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                               LENGTH: 38
TYPE: PRT
                                                                                                                                                             PRIOR APPLICATION NUMBER: PCT/US94/07736
PRIOR TILING DATE: 1994-07-12
PRIOR APPLICATION NUMBER: 60/217,402
PRIOR FILING DATE: 2000-07-11
                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Calenda Valerie
TITLE OF INVENTION: Connective Tissue Growth Factor-2
FILE REFERENCE: PF126P2
                                                                                                          NUMBER OF SEQ
                                                                                                                          PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Li, Haodong
                                                                                                                                             PRIOR APPLICATION NUMBER:
             ORGANISM: homo sapiens
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SEQUENCE DESCRIPTION: ŞEQ ID NO: 2:
3-753-7
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OTHER INFORMATION: "M
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                                                                                                                                                                                                                                                                                                                                                                                                             Adams, Mark
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)S: 8
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LENGTH: 381
TYPE: PRT
ORGANISM: Homo s
                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: US 09/348,815
PRIOR FILING DATE: 1999-07-08
PRIOR APPLICATION NUMBER: US 08/459,101
PRIOR FILING DATE: 1995-06-02
PRIOR APPLICATION NUMBER: PCT/US94/07736
PRIOR FILING DATE: 1994-07-12
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2, Application US/10294796
Publication No. US20030078391A1
GENERAL INFORMATION:
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Matches
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Best Local
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CURRENT FILING DATE: 2002-11-15
                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Li, Haodong et al.
TITLE OF INVENTION: Connective Tissue Growth
FILE REFERENCE: PF126P1D2
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50; Conservative
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CTCIDGAVGCIPLCPQELSLPNLGCPNPRLVKVSGQCCEEWVCDEDSIKDSLDDQDDL---
                                              CTCIDGAVGCIPLCPQELSLPNLGCPNPRLVKVSGQCCEEWVCDEDSIKDSLDDQDDL--
CTCIDGAVGCIPLCPQELSLPNLGCPNPRLVKVSGQCCEEWVCDEDSIKDSHDDQDGLLG
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Pred. No. 1.8e-153;
9; Mismatches 18;
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Pred. No. 1.8e-153;
9; Mismatches 18;
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CURRENT APPLICATION NUMBER: US/09/925,301
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05882
PRIOR APPLICATION NUMBER: PCT/US00/05882
PRIOR APPLICATION NUMBER: 600/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER: OF SEQ ID NOS: 1694
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 1432
LENGTH: 455
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Sequence 1432, Application
Patent No. US20020052308A1
GENERAL INFORMATION:
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                                                CPHPNEASFRLYSLFNDIHKFRD
                                                                                      TYAGCSSVKKYRPKYCGSCVDGRCCTPLQTRTVKMRFRCEDGEMFSKNVMMIQSCKCNYN
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Pred. No. 2.2e-153;
9; Mismatches 18;
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US-10-205-823-84
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Best Local Similarity
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CURRENT FILING DATE: 2002-07-25
PRIOR APPLICATION NUMBER: 60/307,982
PRIOR FILING DATE: 2001-07-25
PRIOR APPLICATION NUMBER: 60/314,356
PRIOR FILING DATE: 2001-08-22
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: FastSEQ for Windows Version 4.0 EQ ID NO 84
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FILING DATE: 2001-12-12
APPLICATION NUMBER: 60/362,158
FILING DATE: 2002-03-05
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                               CPHPNEASFRLYSLFNDIHKFRD 379
                                                            TYAGCLSVKKYRPKYCGSCVDGRCCTPQLTRTVKMRFRCEDGETFSKNVMMIQSCKCNYN
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Kamatkar, Shubhangi
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Gorbatcheva, Bella
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Endege, Wilson O.
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Pred. No. 8.1e-153;
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; SEQUENCE DESCRIPTION: SEQ ID NO: 4: US-10-053-753-4
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Best Local Similarity
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INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
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OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTMARE: PATENTIN PC-DOS/MS-DOS

SOFTMARE: PATENTIN Release #1.0, Version #1.30

CURRENT APPLICATION DATA: Release #1.0, Version #1.30

APPLICATION NUMBER: US/10/053,753

APPLICATION NUMBER: 22-Jan-2002

CLASSIFICATION: <Unknown>

ATTORNEY/AGENT IMPORMATION:

NAME: Clough, David W.

REGISTRATION NUMBER: 36,107
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MEDIUM TYPE: Floppy disk
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357
CPHPNEASFRLYSLFNDIHKFRD 379
                                        TYAGCLSVKKYRPKYCGSCVDGRCCTPQLTRTVKMRFRCEDGETFSKNVMMIQSCKCNYN
                                                                 TYAGCSSVKKYRPKYCGSCVDGRCCTPLQTRTVKMRFRCEDGEMFSKNVMMIQSCKCNYN
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CITY: Chicago
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TOPOLOGY LINEAR

MOLECULE TYPE: PROTEIN

SEQUENCE DESCRIPTION: S
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US-09-853-625B-12
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Best Local Similarity 88.3
Matches 332; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 12, Application US/09853625B Patent No. US20020049304A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER: 33,073
REFERENCE/DOCKET NUMBER: 325800-442
REFERENCE/DOCKET NUMBER: 325800-442
TELECOMMUNICATION INFORMATION: TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 12:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 09/053,587 FILING DATE: <Unknown> ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Hastings, Gregg A. and Adams, Mark D. TITLE OF INVENTION: Human CCN-Like Growth Factor NUMBER OF SEQUENCES: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                121
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                                                                                                                                                                                                     61 NEDCSKTQPCDHTKGLECNFGASSTALKGICRAQSEGRPCEYNSRIYQNGESFQPNCKHQ 120
                           QCSKSCGTGISTRVTNDNPECRLVKETRICEVRPCGQPVYSSLKKGKKCSKTKKSPEPVR 295
                                                                                     ---LGLDASEVELTRNNELIAIGKGSSLKRLPVFGTEPRVLFNPLHÄHGQKCIVQTTSWS 235
                                                                                                                             CTCIGWRRGACIPLCPQELSLPNLGCPNPRLVKVTGQCCEEWVCDEDSIKDPMEDQDGLL 180
                                                                                                                                                CTCIDGAYG-CIPLCPQELSLPNLGCPNPRLYKYSGQCCEEWYCDEDSIKDSLDDQDDL- 178
                                                                                                                                                                                        NEDCRKTOPCDHTKGLECNFGASSTALKGICRAQSEGRPCEYNSRIYQNGESFQPNCKHQ
                                                                                                                                                                                                                                               MSSSTERTLAVAVTLLHLTRLALSTCPAACHCPLEAPKCAPGVGLVRDGCGCCKVCAKQL 60
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CECCHI, STEWART & OLSTEIN
STREET: 6 BECKER FARM ROAD
CITY: ROSELAND
STATE: NEW JERSEY
                                                                      GKGLGFDASEVELTRNNELIAVGKGSSLKRLPVFGMEPRILYNPL--QGQKCIVQTTSWS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: 3.5 INCH DI:
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: AMINO ACID
STRANDEDNESS: <U
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: MULLINS, J.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 374 AMINO ACIDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                    DESCRIPTION: SEQ ID
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88.3%;
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                                                                                                                                                                                                                                                                                                           Score 1819.5; DB 9;
Pred. No. 1.3e-143;
0; Mismatches 27;
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; TYPE: PRT
; ORGANISM: homo s
US-09-901-910-7
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RESULT 10
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SEQ ID NO 7
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: 08/459,101
PRIOR TILING DATE: 1995-06-02
PRIOR APPLICATION NUMBER: PCT/US94/07736
PRIOR FILING DATE: 1994-07-12
PRIOR APPLICATION NUMBER: 60/217,402
PRIOR APPLICATION NUMBER: 60/217,642
PRIOR APPLICATION NUMBER: 60/291,642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILE REFERENCE: PF126P2
CURRENT APPLICATION NUMBER: US/09/901,910
CURRENT FILING DATE: 2001-07-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: 09/348,815 PRIOR FILING DATE: 1999-07-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Adams, Mark
APPLICANT: Calenda Valerie
TITLE OF INVENTION: Connective Tissue Growth Factor-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Li, Haodong
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR FILING DATE: 2001-05-18
                                                                                                                                                                                                                    236 QCSKSCGTGISTRVTNDNPECRLVKETRICEVRPCGQPVYSSLKKGKKCSKTKKSPEPVR 295
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NEDCSKTQPCDHTKGLECNFGASSTALKGICRAQSEGRPCEYNSRIYQNGESFQPNCKHQ 120
                                                                                                                                                                                                                                                                                                GKGLGFDASEVELTRNNELTAVGKGSSLKRLPVFGMEPRILYNPL - - QGQKCIVQTTSWS
                                                                                                                                                                                                                                                                                                                       ---LGLDASEVELTRNNELIAIGKGSSLKRLPVFGTEPRVLFNPLHAHGQKCIVQTTSWS 235
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                                         NCPHPNEASFRLYSLF 371
                                                                                                                       FTYAGCSSVKKYRPKYCGSCVDGRCCTPLQTRTVKMRFRCEDGEMFSKNVMMIQSCKCNY
                                                                                                                                                                                                                                                                                                                                                                                                CTCIGWRRGACIPLCPQELSLPNLGCPNPRLVKVTGQCCEEWVCDEDSIKDPMEDQDGLL 180
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  NCPHANEAAFPFYRLF
                                                                                                FTYAGCLSVKKYRPKYCGSCVDGRCCTPQLTRTVKMRFPCEDGETFSKNVMMIQSSKCNY
                                                                                                                                                                                                QCSKTCGTGISTRVTNDNPECRLVKETRICEVRPCGQPVYSSLKKGKKCSKTKKSPEPVR
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374
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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SEQUENCE CHARACTERISTICS:
LENGTH: 375 AMINO ACIDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 09/053,587
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER: 33,073
REFERENCE/DOCKET NUMBER: 32
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Hastings, Gregg A. and Adams, Mark D. TITLE OF INVENTION: Human CCN-Like Growth Factor NUMBER OF SEQUENCES: 20
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 363 ASFRLYSLFNDIHKFRD 379
                                                                                                       240
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                                                                                                                                                                           187
                                                                                                                                                                                         185 EVELTRNNELIAIGKGSSLKRLPVFGTEP--RVLFNPLHAHGQKCIVQTTSWSQCSKSCG
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                                                     SVKKYRPKYCGSCVDGRCCTPLQTRTVKMRFRCEDGEMFSKNVMMIQSCKCNYNCPHPNE
                                                                                                                       TGISTRVTNDNPECRLVKETRICEVRPCGQPVYSSLKKGKKCSKTKKSPEPVRFTYAGCS
                                                                                                                                                                                                                                                                                                                                                                                                AVAVTLLHLTRLAL-STCPAACHCPLEAPKCAPGVGLVRDGCGCCKVCAKQLNEDCSKTQ
                                   SVKKYRPKYCGSCVDGRCCTPQQTRTVKIRFRCDDGETFTKSVMMIQSCRCNYNCPHANE
                                                                                                       TGISTRVTNDNPDCKLIKETRICEVRPCGQPSYASLKKGKKCTKTKKSPSPVRFTYAGCS
                                                                                                                                                                         EGELTRNNELIAIVKG-GLKMLPVFGSEPQSRAFENP-----KCIVQTTSWSQCSKTCG
                                                                                                                                                                                                                                           GCIPLCPQELSLPNLGCPSPRLVKVPGQCCEEWVCDES---KDALEELEGFFSKEFGLDAS
                                                                                                                                                                                                                                                            GCIPLCPQELSLPNLGCPNPRLVKYSGQCCEEWVCDEDSIKDSLDDQDDL----LGLDAS 184
                                                                                                                                                                                                                                                                                                            PCDHTKGLECNFGASPAATNGICRAQSEGRPCEYNSKIYQNGESFQPNCKHQCTCIDGAV
                                                                                                                                                                                                                                                                                                                                              PCDHTKGLECNFGASSTALKGICRAQSEGRPCEYNSRIYQNGESFQPNCKHQCTCIDGAV 128
                                                                                                                                                                                                                                                                                                                                                                                ALAAALLCLARLALGSPCPAVCQCPAAAPQCAPGVGLVPDGCGCCKVCAKQLNEDCSRTQ
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STATE: NEW JERSEY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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80.1%;
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Pred. No. 3.2e-129;
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& OLSTEIN
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US-10-101-040-3
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                                                                                                                                                                                      Sequence 3, Application US/10101040 Publication No. US20020142353A1
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                                            APPLICANT: FIBROGEN, INC
APPLICANT: SCHMIDT, Brian
APPLICANT: ALLEN, Margaret
APPLICANT: SVERDRUP, Fran
APPLICANT: CARMICHAEL, David
TITLE OF INVENTION: CONNECTIVE TISSUE GROWTH FACTOR (CTGF) AND METHODS
TITLE OF INVENTION: USE
                                 FILE REFERENCE: FIBRO1100-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
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APPLICATION NUMBER: US/10/101,040 FILING DATE: 2002-03-18
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ORGANISM: Rattus norvegicus US-10-245-977-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: US 60/323,305
PRIOR FILING DATE: 2001-09-18
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn version 3.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Usinger, William R
TITLE OF INVENTION: METHODS OF ASSAYING CONNECTIVE TISSUE GROWTH FACTOR
FILE REFERENCE: FP0812 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Weitz, Stephen L APPLICANT: Usinger, William
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PGDNDIFESLYYRKMYGDM 346
                                               PHPNEASFRLY -- SLFNDI 374
                                                                                                                                                                                                                            SKSCGTGISTRVTNDNPECRLVKETRICEVRPCGQPVYSSLKKGKKCSKTKKSPEPVRFT
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                                                                                                   LSGCTSVKTYRAKFCGVCTDGRCCTPHRTTTLPVEFKCPDGEIMKKNMMFIKTCACHYNC
                                                                                                                                                                                                  SKTCGMGISTRVTNDNTFCRLEKQSRLCMVRPCEADLEENIKKGKKCIRTPKIAKPVKFE
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Pred. No. 4.3e-72;
1; Mismatches 104;
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; LENGTH: 348
; TYPE: PRT
; ORGANISM: Mouse
US-10-101-040-3
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US-09-853-625B-15
; Sequence 15, Application US/09853625B
; Patent No. US20020049304A1
; GENERAL INFORMATION:
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Best Local
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PRIOR FILING DATE: 1998-11-06
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PatentIn version 3.0
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                 COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/853,625B
FILING DATE: 14-May-2001
CLASSIFICATION: <Unknown>
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     PRIOR APPLICATION DATA:
                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Human CCN-Like Growth NUMBER OF SEQUENCES: 20
                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Hastings, Gregg A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  178;
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                                                                                                                                                                                                                                  CITY: ROSELAND
STATE: NEW JERSEY
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CECCHI, STEWART 6 OLSTEIN
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US-10-053-753-6
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                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                APPLICANT: Lau, Lester F. TITLE OF INVENTION: Extracellular Matrix Signalling Molecules NUMBER OF SEQUENCES: 17
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                                                                                                                                                    STREET: 6300 Sears
CITY: Chicago
STATE: Illinois
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CPHPNEASFRLY -- SLFNDI 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CSKTCGMGISTRVTNDNTFCRLEKQSRLCMVRPCEADLEENIKKGKKCIRTPKIAKPVKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CSKSCGTGISTRVTNDNPECRLVKETRICEVRPCGQPVYSSLKKGKKCSKTKKSPEPVRF 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LLGLDASEVELTRNNELIAIGKGSSLKRL-PVFGTEPRVLFNPLHAHGQKCIVQTTSWSQ 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KHQCTCIDGAVGCIPLCPQELSLPNLGCPNPRLVKVSGQCCEEWVCDEDSIKDSLDDQDD 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MLASVAGPISLALVLLALCTRPATGQDCSAQCQCAAEAAPHCPAGVSLVLDGCGCCRVCA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----RANCLYQTTEWSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KQLGELCTERDPCDPHKGLFCDFGSPANRKIGVCTAK-DGAPCVFGGSVYRSGESFQSSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 348 AMINO ACIDS
TYPE: AMINO ACID
                                                                                                                   ZIP: 60606-6402
                                                                                                                                   COUNTRY: United States of America
                                                                                                                                                                                                          ADDRESSEE: Marshall,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: 201-994-17
TELEFAX: 201-994-1744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER: 33,073
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: MULLINS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 09/053,587
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO: 15:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61;
                                                                                                                                                                                          Tower,
                                                                                                                                                                                        , O'Toole,
Fower, 233
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                                                                                                                                                                                            South Wacker Drive
                     Version
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39;

Gaps

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267

APPLICATION NUMBER: US/10/053,753

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RESULT 15
US-10-245-977-8
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                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                 Sequence 8, Application US/10245977 Publication No. US20030113816A1
                                    APPLICANT: Weitz, Stephen L
APPLICANT: Weitz, Stephen R
APPLICANT: Usinger, William R
TITLE OF INVENTION: METHODS OF ASSAYING CONNECTIVE TISSUE GROWTH FACTOR
FILE REFERENCE: FP0812 US
CURRENT APPLICATION NUMBER: US/10/245,977
CURRENT FILING DATE: 2002-09-18
PRIOR APPLICATION NUMBER: US 60/323,305
PRIOR APPLICATION DATE: 2001-09-18
NUMBER OF SEQ ID NOS: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 177; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                      SOFTWARE:
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ID NO 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 312/474-0448
TELEX: 25-3856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc_feature
OTHER INFORMATION: "Fispl2
SEQUENCE DESCRIPTION: SEQ ID NO: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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                      PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                    CPGDNDIFESLYYRKMYGDM 347
                                                                                                                                                                                                                                                                                                                                                                                        CPHPNEASFRLY -- SLFNDI 374
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KHQCTCIDGAVGCIPLCPQELSLPNLGCPNPRLVKVSGQCCEEWVCDEDSIKDSLDDQDD 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KQLNEDCSKTQPCDHTKGLECNFGASSTALKGICRAQSEGRPCEYNSRIYQNGESFQPNC 117
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STRANDEDNESS: single
TOPOLOGY: linear
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LENGTH: 348 amino acids
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Search completed: August Job time: 36.4092 secs

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Best Local Similarity
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                                                                                                                         LLGLDASEVELTRNNELIAIGKGSSLKRL-PVFGTEPRVLFNPLHAHGQKCIVQTTSWSQ 236
CPGDNDIFESLYYRKMYGDM 347
                                                               ELSGCTSVKTYRAKFCGVCTDGRCCTPHRTTTLPVEFKCPDGEIMKKNMMFIKTCACHYN 327
                                                                                                                                                                                                                                                            KYQCTCLDGAVGCVPLCSMDVRLPSPDCPFPRRVKLPGKCCKEWVCDEP-------
                             CPHPNEASFRLY -- SLFNDI 374
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           45.3%;
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Pred. No. 1.5e-
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Minimum
Maximum
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Gapop 10.0 , Gapext 0.5
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T42218
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A40557
A40551
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I38069
I726972
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T13954
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h prot
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RESULT 1 A35669 gene CYR61 C;Species; C;Date: 28- C;Accession R;O'Brien, Mol. Cell. A;Title: Ex A;Reference A;Accession A;Status: p A;Molecule		44	44	44	41	40	39	38	37	ນຕ	34	ယ္အ	32	31	30	
RESULT 1 A35669 Gene CYR61 protein precursor - mouse C;Species: Mus musculus (house mouse) C;Date: 28-Sep-1990 #sequence_revision. C;Accession: A35669; I48319; S16446 R;O'Brien, T.P.; Yang, G.P.; Sanders, I MOI. Cell. Biol. 10, 3569-3577, 1990 A;Fitle: Expression of Cyr61, a growth A;Reference number: A35669; MUID:902871 A;Accession: A35669 A;Status: preliminary A;Molecule type: mRNA		131.5	130	132.5	132.5	133	133	133.5	133.5	133.5	134	135	.135	135	135.5	
rotein precius musculus musculus ep-1990 #se A35669; I4 .P.; Yang, Lol. 10, 35 rression of number: A35669 A35669 eliminary ype: mRNA		6.3	י פיע		, σ . ω	6.3	6.3	6. ₃	σ. ω.	n σ . ω	6.4	6.4	6.4		6.4	
protein precursor - Mus musculus (house Sep-1990 #sequence_r Sep-1990 #sequence_r T.P.; Yang, G.P.; Sa Biol. 10, 3569-3577, Brossion of cyr61, a pression of cyr61, a		810	1292	1106	884	2531	1220	3002	2555	305	2219	3704	3672	1523	305	
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e e) ion 18-Nov-1992 s, L.; Lau, L.F. 0 wth factor-induc 287146; PMID:235	ALIGNMENTS	T10756	T09229	T13938	T18649	S18188	A56136	A47221	A40043	JN0508	T27684	T37316	T23433	T13953	148601	
<pre>#text_change 05-Nov-1999 ible immediate-early gene. 5916</pre>		Nel-homolog protei	galactose binding	hynothetical prote	hypothetical prote	notch protein homo	jagged protein pre	fibrillin 1 precur	notch protein homo	insulin-like growt	hypothetical prote	probable laminin a	hypothetical prote	MEGF5 protein - ra	insulin-like growt	

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Db 181 LDASEVELTRNNELIAIGKGSSLKRLPVFGTEPRVLENPLHAHGQKCIVQTTSWSQCSKS 240	QY 181 LDASEVELTRNNELIAIGKGSSLKRLPVFGTEPRVLFNPLHAHGQKCIVQTTSWSQCSKS 240	Db 121 CTCIDGAVGCIPLCPQELSLPNLGCPNPRLVKVSGQCCEEWVCDEDSIKDSLDDQDDLLG 180	QY 121 CTCIDGAVGCIPLCPQELSLPNLGCPNPRLVKVSGQCCEEWVCDEDSIKDSLDDQDDLLG 180	Db 61 NEDCSKTQPCDHTKGLECNFGASSTALKGICRAQSEGRPCEYNSRIYQNGESFQPNCKHQ 120	QY 61 NEDCSKTQPCDHTKGLECNFGASSTALKGICRAQSEGRPCEYNSRIYQNGESFQPNCKHQ 120	Db 1 MSSSTERTLAVAVTLLHLTRLALSTCPAACHCPLEAPKCAPGVGLVRDGCGCCKVCAKQL 60	Qy 1 MSSSTERTLAVAVTLLHLTRLALSTCPAACHCPLEAPKCAPGVGLVRDGCGCCCKVCAKQL 60	Query Match 100.0%; Score 2103; DB 2; Length 379; Best Local Similarity 100.0%; Pred. No. 1.5e-141; Matches 379; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	C;Supertanily: von Willebrand factor type C repeat homology <vwc> F;99-166/Domain: von Willebrand factor type C repeat homology <vwc></vwc></vwc>	A;Gene: CYR61 A;Gene: CYR61 A;Introns: 21/3; 93/1; 208/1; 279/3	A; Note: the authors translated the codon GAT for residue 337 as Gln	A; Closs references: Embl: A50/90; NID: 950032; FID: CARAVIOS.; FID: 950033 A; Note: the authors did not translate the codon for residue 108	A; Residues: 1-379 < RES>	A; Scatus: translated from GB/EMBL/DUBJ A: Molecule type: DNA A: Molecule type: DNA	A; Accession: 148319	A; Reference number: 148319; MUID:91288203; PMID:2062642	Nucleic Acids Res. 19, 3261-3267, 1991	R; Latinkic, B.V.; O'Brien, T.P.; Lau, L.F.	A; Note: the authors translated the codon GAT for residue 337 as Gln	A;Residues: 1-379 <uab> A;Cross-references: GB:M32490; NID:q192909; PIDN:AAA37512.1; PID:q309206 .</uab>	

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RESULT 3
A40578
beta IG-M2 protein precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 06-Mar-1992 #sequence_revision 06-Mar-1992
C:Accession: A40578; A53228
R:Brunner, A.; Chinn, J.; Mubauer, M.; Purchio, A.:
DNA Cell Biol. 10, 293-300, 1991
A:Title: Identification of a gene family regulated |
A;Reference number: A40578; MUID:91229699; PMID:202
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Species: Gallus gallus (chicken)
C;Date: 03-Apr-1992 #sequence_revision 03-Apr-1992 #text_change 21-Jul-2000
C;Accession: A41428
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                                                                                                                                                                                                            ASFRLYSLFNDIHKFRD
                                                                                                                                                                                                                                         SVKKYRPKYCGSCVDGRCCTPQQTRTVKIRFRCDDGETFTKSVMMIQSCRCNYNCPHANE
                                                                                                                                                                                                                                                        SVKKYRPKYCGSCVDGRCCTPLQTRTVKMRFRCEDGEMFSKNVMMIQSCKCNYNCPHPNE
                                                                                                                                                                                                                                                                                                  TGISTRVTNDNPDCKLIKETRICEVRPCGQPSYASLKKGKKCTKTKKSPSPVRFTYAGCS
                                                                                                                                                                                                                                                                                                                   TGISTRVTNDNPECRLYKETRICEVRPCGQPVYSSLKKGKKCSKTKKSPEPVRFTYAGCS
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                                                                                                                                                                                                                                                                                                                                                                        EVELTRNNELIAIGKGSSLKRLPVFGTEP--RVLFNPLHAHGQKCIVQTTSWSQCSKSCG
                                                                                                                                                                                                                                                                                                                                                                                                                 GCIPLCPQELSLPNLGCPNPRLVKVSGQCCEEWVCDEDSIKDSLDDQDDL----LGLDAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PCDHTKGLECNFGASPAATNGICRAQSEGRPCEYNSKIYQNGESFQPNCKHQCTCIDGAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PCDHTKGLECNFGASSTALKGICRAQSEGRPCEYNSRIYQNGESFQPNCKHQCTCIDGAV
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80.1%;
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Pred. No. 2.9e-109;
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                                                                         06-Mar-1992 #text_change
 regulated by transforming
9; PMID:2029337
                                            A.F.
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A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-349 <OEN
A;Cross-references: EN
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C;Species: Homo sapiens (man)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change
C;Accession: A4051; S44205
R;Bradham, D.M.; Igarashi, A.; Potter, R.L.; Grotendorst, G.R.
J. Cell Biol. 114, 1285-1294, 1991
A;Title: Connective tissue growth factor: a cysteine-rich mitoge
A;Reference number: A40551; MUID:91373462; PMID:1654338
                                                                                                                A;Cross-references: GB:M92934; GB:M36965; GB:S56201; NID:g180923; PIDN:AAA91279. R;Oemar, B.S.; Werner, A.; Yang, Z.; Garnier, J.M.; Gentz, R.; Luescher, T.F. submitted to the EMBL Data Library, April 1994
A;Description: Differential cloning and expression of human connective tissue gr
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A;Title: Structure, mapping, and expression of fisp-12, a gro A;Reference number: A53228; MUID:91363390; PMID:1888698
A;Accession: A53228
                                                                   A; Reference number: A; Accession: S44205
                                                                                                                                                                                                                 A; Molecule type: mRNA
A; Residues: 1-349 <BRA>
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A; Residues: 1-160, 'K', 162-348 <
A; Cross-references: GB:M70641;
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A; Residues: 1-348 < BRU>
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^OEM>
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No. 1.4
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EMBL: X78947; NID: g474933;

PID:g474934

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NOV protein - chicken
C;Species: Gallus gallus (chicken)
C;Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jul-2000
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R;JOLIOt, V.; Martinerie, C.; Dambrine, G.; Plassiart, G.; Brisac, M.; Crochet, C., Mol. Cell. Biol. 12, 10-21, 1992

A;Title: Proviral rearrangements and overexpression of a new cellular gene (nov) A;Reference number: S20078; MUID:92107157; PMID:1309586

A;Accession: S20078
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A; Residues: 1-351 <JOL>
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Best Local Similarity
Matches 176; Conserv
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nes 165; Conserv
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                                                                                                                  TCIDGAVGCIPLCPQELSLPNLGCPNPRLVKVSGQCCEEWVCD-EDSI-----KDSLDDQ
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 QCSKSCGTGISTRVTNDNPECRLVKETRICEVRPCGQPVYSSLKKGKKCSKTKKSPEPVR
                                   EATLGIDVSD
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44.5%; Pred. No. 9.6e-54;
tive 44; Mismatches 110;
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45.7%; Pred. No. 4.8e-60;
tive 64; Mismatches 97;
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A;Title: Structural analysis of the human nov proto-oncogene
A;Reference number: I38069; MUID:94336229; PMID:7520150
A;Recession: I38069
A;Status: preliminary; translated from GB/EMBL/DDBJ
hypothetical protein Y47H9C.4 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 17-Mar-2000 C;Accession: T26972 R;Harris, B.
                                                                                RESULT 7
T26972
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C;Species: Homo sapiens (man)
C;Date: 17-May-1996 *sequence_revision 17-May-1996 *text_change
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C;Superfamily: thrombospondin type 1 repeat homology
F;203-250/Domain: thrombospondin type 1 repeat homology
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A; Residues: 1-357 < RES>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Cross-references: EMBL: X78351; NID: g587422; PIDN: CAA55146.1; PID: g825696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R; Martinerie, C.; Huff, V.; Joubert, I.; Badzioch, M.; Saunders, G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C; Accession: I38069
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                I38069
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MSSSTF----RTLAVAVTLLHLTRLALST--CPAAC--HCPLEAPKCAPGVGLVRDGCGC
                                                                                                                                                                  KCNYNCPHPNEA 363
                                                                                                                                                                                                         RAIHLQFKNCTSLHTYKPRFCGVCSDGRCCTPHNTKTIQAEFQCSPGQIVKKPVMVIGTC
                                                                                                                                                                                                                                                                                                                                                           DDQDDLLGLDASEVELTRNNELIAIGKGSSLKRLPVFGTEPRVLFNPLHAHGQKCIVQTT 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CKVCAKQLNEDCSKTQPCDHTKGLECNFGASSTALKGICRAQSEGRPCEYNSRIYQNGES 112
                                                                                                                                                  TCHTNCPKNNEA
                                                                                                                                                                                                                                                                            EWTACSKSCGMGFSTRVTNRNRQCEMLKQTRLCMVRPCEQEPEQPTDKKGKKCLRTKKSL
                                                                                                                                                                                                                                                                                                                                                                                                                         FQPNCKHQCTCIDGAVGCIPLCPQELSLPNLGCPNPRLVKVSGQCCEEWVCDEDSIKDSL 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLVCARQRGESCSDLEPCDESSGLYCDRSADPSNQTGTCTA-VEGDNCVFDGVIYRSGEK 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VQSTSFCLRKQCLCLTFLLLHLLGQVAATQRCPPQCPGRCPATPPTCAPGVRAVLDGCSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACSKSCGMGFSTRVTNRNQQCEMVKQTRLCMMRPCENEEPSD-KKGKKCIQTKKSMKAVR
                                                                                                                                                                                                                                            EPVRFTYAGCSSVKKYRPKYCGSCVDGRCCTPLQTRTVKMRFRCEDGEMFSKNVMMIQSC
                                                                                                                                                                                                                                                                                                          SWSQCSKSCGTGISTRVTNDNPECRLVKETRICEVRPCGQ-PVYSSLKKGKKCSKTKKSP 291
                                                                                                                                                                                                                                                                                                                                            GG----LTLAAYRPEATLGVEV----SDSSV-----NCIEQTT
                                                                                                                                                                                                                                                                                                                                                                                                            FQPSCKFQCTCRDGQIGCVPRCQLDVLLPEPNCPAPRKVEVPGECCEKWICGPDE-EDSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCPQSNNAFFQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 839.5; Depred. No. 3.2e-52; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3.2e-52;
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Length <THR1>

357 41;

Gaps

9;

63

181

271

211

and

expression

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Wilms Perb

Strong,

05-Nov-1999

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mucin - rat
C;Species: Rattus norvegicus (Norway rat)
C;Species: Partus norvegicus (Norway rat)
C;Date: 23-Sep-1997 #sequence_revision 23-Sep-1997 #text_change 05-Nov-1999
C;Accession: JC5598
C;Accession: JC5598 A S : Zhan, Q.; Spurr-Michaud, S.; Gipson, I.K.
                                                                    A; Note: translation not complete C; Comment: This protein is a high molecular weight ntestinal tract and reproductive tract.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status. F.~—
A;Molecule type: DNA
A;Residues: 1-1111 <WIL>
A;Cross-references: EMBL:AL032657; F
A;Cross-references: Clone Y47H9C
C; Superfamily: vc F; 45-149/Domain:
                                                                                                                                                                                                                         R;Inatomi, T.; Tisdale, A.S.; Zhan, Q.; Spurr-Michaud, S.; Gipson, Biochem. Biophys. Res. Commun. 236, 789-797, 1997
A;Title: Cloning of rat Muc5AC mucin gene: Comparison of its struct A;Reference number: JC5598; MUID:97396181; PMID:9245735
                                                                                                                                                                                                                                                                                                                                                                                  RESULT
JC5598
                                       A; Gene:
                                                                                                                                                   A; Molecule type: mRNA
A; Residues: 1-1034 <INA>
                                                                                                                               A;Cross-references: GB:U83139; NID:g2315984; PIDN:AAC53312.1; PID:g2315985
                                                                                                                                                                                          A; Status: nucleic acid sequence not shown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           submitted to the EME
A; Reference number:
A; Accession: T26972
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Status: preliminary; translated
                                                        Genetics:
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number: Z20293
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NYNCPHPN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TNDNPECRLVKETRICEVRPCGQPVYSSLKKGKKCSKTKKSPEPVRFTY------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LIAIGKGSSLKRLPVFGTEPRVLFNPLHAHGQKCIVQ-TTSWSQCSK---SCGTGISTRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SYGPGCKLHCKCVNGKCDKETGEC----TC-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NFGASSTALKGICRAQSEGRPCEYNSRIYQNGESFQPNCKHQCTC-----IDGA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SSVKKYRPKYCGSCVDGRCCTPLQTRTV-----
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von Willebrand factor
n: cysteine-rich <CYS>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8.1%; Score 171; DB 2;
20.1%; Pred. No. 0.00016;
Live 32; Mismatches 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Library, October 1998
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               type
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -YGESCELSCPCSDASCSKQTGKCLCPLGTKG
                 repeat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -KMRFRCEDGEMFSKNVMMIQSCKC
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                                                                                          glycoprotein which
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99; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                 CHCPLEAPKCAPGVGLVRDGCGCCKVC---AKQLNEDCSKT----QPCDHTKGLECN
                                                                                 KGKKCSKTKKSPEPVRFTYAGCSSVKKYRPKYC-GSCVDG--
                                                                                                                                            RLVKE----
                                                                                                                                                                                                                               NSSHCPPPLHCPESSSLIVTYEEGTCCPSQNCSSQKGCDVNGT----LYQPGDVVSSSLC
                                                                                                                                                                                                                                                                                                                                           RNDDISLSLATQKAGPKSEGCFCPDDMTLFSSNDSICVPSCQWCLGPHGEPVEPGHTISI
                                                                                                                                                                                                                                                                                                                                                                        FGASSTALKGICRA - - QSEGRPCEYNSRIYQ -
                                                                                                                                                                                                                                                                                                                                                                                                     CHM-LDLEVVCSGLELYASLCAAQGVCIPWRSHTNNTCPFTCPENQVYQPCGPSNPHYCY
LQTSQRSVTLHCDDGSSRTFSYTQVEKCGCLGQRCHAPGDTS
                         LQTRTVKMRFRCEDGEMFSKNVMMIQSCKC-NYNCPHPNEAS
                                                       PQQKCTVHQRQ-QIIR--QQNCSSEGPVSLSYCQGNCGDSTSMYSLEANTVEHTCECCQE
                                                                                                               SLYKPGEFWPEPGNPCVTHKCEKFQDVLTVVTVKIECPKINCPQDWAQLREDGCCYDCLV
                                                                                                                                                                       ERCLCEVSSNAFSDVFVVNCETELCNTQCPKGFEYQTTPGHCCGQCVPKTCPFKNSNNST
                                                                                                                                                                                                    QKCIVQTTS:
                                                                                                                                                                                                                                                          DSLDDQDDLLGLDASEVELTRNNELIAIGKG-SSLKRLPVFGTEPRVLFNP----LHAHG
                                                                                                                                                                                                                                                                                       NCQ-DCICKEGTLTCQEKLCPQPT---
                                                                                                                                                                                                                                                                                                                NCKHQCTCIDGAVGC-IPLCPQELSLPNLGCPNPRLVKVS-----GQCCEEWVCDEDSIK 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21.4%;
                                                                                                                                            -TRICE-----VR-----PCGQP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                              47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 166;
Pred. No. 0.
                                                                                                                                                                                                  -WSQCSKSCGTGISTRVT----
                                                                                                                                                                                                                                                                                                                                                                                                                                                              ed. No. 0.00035;
Mismatches 170;
                                                                                                                                                                                                                                                                                       -CPEPGFVPVSIALEAGQCCSQFSC----VC
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1000
                           364
                                                                                                                                                                                                                                                                                                                                                                          -NGESFQP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                              146;
                                                                                                                                          -VYSSLK 279
                                                                                  -RCCTP
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A;Molecule type: mRNA
A;Residues: 12139-12167,'T',12169-13288 <EC3>
A;Residues: 12139-12167,'T',12169-13288 <EC3>
A;Cross-references: GB:M61883; NID:g454837; PIDN:AAA30998.1; PIR:Timpte, C.S.; Eckhardt, A.E.; Abernethy, J.L.; Hill, R.L.
J. Biol. Chem. 263, 1081-1088, 1988
A;Title: Porcine submaxillary gland apomucin contains tandemly
A;Reference number: A28528; MUID:88087170; PMID:2826455
                                                                                                                                                                                                                                                                                               A;Cross-references: EMBL:AF005273; NID:g2581863; PIDN:AAC62527.1; PID:g2581864 R;Eckhardt, A.E.; Timpte, C.S.; Abernethy, J.L.; Zhao, Y.; Hill, R.L. J. Biol. Chem. 266, 9678-9686, 1991 A;Title: Porcine submaxillary mucin contains a cystine-rich, carboxyl-terminal A;Reference number: A40009; MUID:91236743; PMID:2033060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Eckhardt, A.E.; Timpte, C.S.; DeLuca, A.W.; Hill, R.L. J. Biol. Chem. 272, 33204-33210, 1997
A;Title: The complete cDNA sequence and structural polymorphism A;Reference number: Z14839; MUID:98070526; PMID:9407109
A;Accession: T03099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Sus scrofa domestica (domestic pig)
C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999
C;Accession: T03099; A40009; A28528; B29789
                                                                                                                                                                                                                                                                    A; Accession: A40009
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A;Residues: 1-13288 <ECK>
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                                                                                                                                                       PID:g164374
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A;Molecule type: mRNA
A;Residues: 12139-12167,'T',12169-12641 <TIM>
A;Residues: 12139-12167,'T',12169-12641 <TIM>
A;Cross-references: GB:M21174; GB:J03512; NID:g164321; PIDN:AAA30990.1;
A;Experimental source: submaxillary gland
R;Eckhardt, A.E.; Timpte, C.S.; Abernethy, J.L.; Toumadje, A.; Johnson J

Jr.

W.C.;

Hil

PID:g552360

S)

A; Accession: A28528

Query Match 7.4%; Score 156.5; DB 2; Length 1574; Best Local Similarity 20.4%; Pred. No. 0.0024; Matches 94; Conservative 40; Mismatches 142; Indels 185; Gaps 24; Qy 26 CPAACHCPLEAPKCAPGVGLVRDGC	C:Species: Rattus norvegicus (Norway rat) C:Species: Rattus norvegicus (Norway rat) C:Species: Rattus norvegicus (Norway rat) C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 21-Jul-2000 C:Accession: T13554 R:Rakayama, M.; Nakajima, D.; Nagase, T.; Nomura, N.; Seki, N.; Ohara, O. Genomics 51, 27-34, 1998 A;Title: Identification of high-molecular-weight proteins with multiple EGF-like motifs A;Reference number: Z14126; MUID:98360089; PMID:9693030 A;Accession: T13954 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Status: preliminary; translated from GB/EMBL/DDBJ A;Residues: 1-1574 <nak> A;Residues: 1-1574 <nak> A;Cross-references: EMBL.AB011532; NID:93449293; PIDN:BAA32462.1; PID:g3449294 A;Experimental source: strain Sprague-Dawley; brain C:Genetics: A;Gene: MEGF6</nak></nak>	221 Hz 1052 RP 1052 RP 256 CF 11112 CR 303 SV 11163 AV 1163 AV 1220 GC	J. Biol. Chem. 262, 11339-11344, 1987 A;Title: Structural properties of porcine submaxillary gland apomucin. A;Reference number: A92606; MUID:87280230; PMID:3611111 A;Accession: B29789 A;Molecule type: protein A;Residues: 1572-1607 <ec2> C;Superfamily: pig submaxillary mucin C;Superfamily: pig</ec2>
OY 166 DSIKDSLDDQDDLLGDDASEVELTKNELLALGKGSSLKKLLVYGTERVLKNELHANG 223 Db 1207	Matches 92; Conservative 27; Mismatches 134; Indels 143; Gaps 26 CPAACHCPLEAP	al protein Y64G10A.f - Caenorhabditis elegans Caenorhabditis elegans -Oct-1999 #sequence_revision 15-Oct-1999 #tex h, R. to the EMBL Data Library, September 1999 e number: Z20336 n: T27283 preliminary; translated from GB/EMBL/DDBJ type: DNA type:	Oy 51 GCCKYCAKQLNEDCSKTOPCDHTKGLECNFGASSTALKGICR 92

Qy 348 IQSCKC 353 : Db 1015 VVKCGC 1020	955 RDYYQKQQGYAACQTTKKVSRLECRGGCAGGQCCGFLRSKRRKYSFECTDGSSFVDEVEK	QY 295 RFTYAGCSSVKKYRPKYC-GSCVDGRCCTPLQTRTVKMRERCEDGEMFSKNVMM 347	Db 896 GHGGVICDEEEDLFNP-CQMIKCKHGKCRLSGVGQPYCECNSGFTGDSCDREISCRGERI 954	253NPECRLVK-ETRICEVRPCGQPVYSSLKKGKKCSK-TKKSPEPV	Db 836 VCAHGMCQPSSQSGFTCECEEGWMGPLCDQRTNDPCLGNKCVHGTCLPINAFSYSCKCLE 895		Db 776 YVGGMPGKNNVASLRQAPGQNGTSFHGCIRNLYINSELQDFRKMPMQTGILPGCEPCHKK 835	Qy 221 HAHGHG			Db 656 VSVNFVNKESYLQIPSAKVRPQTNITLQIATDEDSGILLYKGDKDHIAVELYRGRVRASY 715	QY 162 VCDEDSIKDSLDDQDDLLGLDASEVELTRNNELIAI 197	Db 596 CVCPEGYSGLFCEFSPPMVLPRTSPCDNFDCQNGAQCIIRINEPICQCLPGYLGEKCEKL 655	QY 132 PLCPQELSLPNLGCPNPRLVKVSGQCCEEW 161	Db 552 TPKGFKCDCTPGYIGEHCDIDFDDCQDNKCKNGAHCTDAVNGYT 595	Qy 73 -TKGLECNFGASSTALKGICRAQSEGRPCEYNSRIYQNGESFQPNCKHQCTCIDGAVGCI 131	Db 507 STCVDGINNYTCLCPPEYTGELCEEKLDFCAQDLNPCQHDSKCIL 551	QY 24 STCPAACHCPLEAPKCAPGVGLVRDGCGCCKVCAKQLNEDCSKTQPCDH 72	101; Conservative 47;	Query Match 7.4%; Score 156; DB 2; Length 1025; Best Local Similarity 18.5%; Prod. No. 0.0018;	C;Superfamily: fruit fly slit protein; EGF homology; leucine-rich alpha-2-glycoprotein r	A;Residues: 1-1025 <hol> A;Residues: 1-1025 <hol> A;Cross-references: EMBL:AF074960; NID:g4151258; PID:g4151259; PIDN:AAD04345.1 C;GenetLos: A;Cross-cit-2</hol></hol>	A.Status: preliminary; translated from GB/EMBL/DDBJ A.Molocule type: mpna A.Molocule type: mpna	A; Title: Distinct but overlapping expression patterns of two vertebrate slit homologs in A; Reference number: Z22177; MUID:99279238; PMID:10349621	ge, L.; Raman, S.; Algar, E.; Yamada, T	ion: T42626	ate names: neurogenic extracellular slit protein s: Mus musculus (house mouse) 11-17an 2000 #secusoro rovision 11-17an 2000 #tovt change 16-	742626 Secreted leucine-rich repeat-containing protein SLIT2 - mouse (fragment)		Db 1347 CTELCPDG-TFGESCSQKCDCGEN 1369	1293 CSCQPGWRGKKCNRPCLKGYFGRHCSQSCRC	
RESULY 14 A53767 mucin MUC5B, tracheobronchial – human C;Species: Homo sapiens (man) C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 20-Apr-2000 C;Accession: A53767		Db 904 EVEECGCMGRRCPAPGD 920	QY 347 MIQSCKC-NYNCPHPNE 362	844 SSEPVRLAYCRGNCGDSSSMYSLEGNTVEHRCQCCQELRTSLRNVTLHCTDGSSRAFSYT	Qy 303 SVKKYRPKYC-GSCVDGRCCTPLQTRTVKMRFRCEDGEMFSKNVM 346		Qy 287TKKSPEPVRFRFTYAGCS 302	Db 724 THCPVGFEYQEQSGQCCGTCVQVACVTNTSKSPAHLFYPGETWSDAGNHCVTHQCEKHQD 783	267 VKRCSK	665	Qy 223 HGQKCIVQTTSWSQCSKSCGTGISTRVTNDNPECRLVKETRICE 266	Db 641ACNTSRCPAPVGCPEGARAIPTYQ 664	QY 164 DEDSIKDSLDDQDDLLGLDASEVELTRNNELIAIGKGSSLKRLPV-FGTEPRVLFNPLHA 222	Db 587 TVGMDCQ-ECTCEAATWTLTCRPKLCPLPP-ACPLPGFVPVPAAPQAGQCCPQYSC 640	QY 112 SFQPNCKHQCTCIDGAVGCIP-LCPQELSLPNLGCPNPRLVKVSGQCCEEWVC 163	Db 528 YC-YGNDSASLGALPEAGPITEGCFCPEGMTLFSTSAQVCVPTGCPRCLGPHGEPVKVGH 586	QY 77 ECNEGASSTALKGICRAQSEGRPCEYNSRIYQNGE 111	Db 468 VFDRCHMTDLDVVCSSLELYAALCASHDICIDWRGRTGHMCPFTCPADKVYQPCGPSNPS 527	Qy 53CKYCAKQLNEDCSKTQPCDHTKGL 76 .	Db 411 TTVGSTTVGFTTVGSTTVGFTTPPAPCLPSPICHLILSKVFEPCHTVIPPLLFYEGC 467	Qy 4 STERTLAVAVTLLHLTRLALSTCPAACHCPLEAPKCAPGVGLVRDGCGC 52	Query Match 7.3%; Score 152.5; DB 2; Length 1042; Best Local Similarity 18.9%; Pred. No. 0.0032; Matches 105; Conservative 48; Mismatches 159; Indels 245; Gaps 27;	F;678-746/Domain: von Willebrand factor type C repeat homology <vwc></vwc>	A;Cross-references: GDB:454136; OMIW:158373 A;Cross-references: GDB:454136; OMIW:158373	Genetics: Gene: GDB:MUC5AC	Cross-references	Statu	A;TILLE: CHAIRCHEITZALION OF A MUID: 95293957; PMID:7775418 A;Reference number: A57534; MUID:95293957; PMID:7775418 A;Accession: A57534	fleur, T.; Roche, F.; Hill, A.S.; Lacasa, M.; Fox, M.; Swallow, D.M.; Zweibau . Chem. 270, 13665-13673, 1995 . Chem. 270, 13665-13673, 1995	change 20-Apr-2000	7534 cin 5A	RESULT 13

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Balbiani ring 3 protein - midge (Chironomus tentans)
(;Species: Chironomus tentans
C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 21-Jul-2000
C;Accession: S08167
R;Paulsson, G: Lendahl, U: Galli, J: Ericsson, C: Wieslander, L.
J. Mol. Biol. 211, 331-349, 1990
A;Title: The balbiani ring 3 gene in Chironomus tentans has a diverged repetitive
A;Reference number: S08167; MUID:90172404; PMID:1689777
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A;Molecule type: mRNA
A;Residues: 1-1056 <MEE>
A;Cross-references: GB:U06711; NID:g488072; PIDN:AAA18431.
A;Cross-references: GB:U06711; NID:g488072; PIDN:AAA18431.
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A;Title: Cloning and analysis of cDNA encoding a major airway glycoprotein, human trached A; Reference number: A53767; MUID:94230376; PMID:7513696
A;Accession: A53767
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A;Map position: 11p15.5-11p15.5
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F;767-835/Domain: von Willebrand factor type C repeat homology
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Best Local
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Pred. No. 0.0035;
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Search completed: August Job time: 17.4592 secs

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627 303 579 530

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A;Status: not compared with conceptual translation A;Molecule type: DNA A;Molecule type: DNA A;Residues: 1-1700 <PAU> A;Cross-references: GB:X52263; NID:g7057; PIDN:CAA36506.1; PID:g7058 C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30 CHCPLEAPKCAPGVGLYRDGCG--C-CKVCAKQLNEDCSKTQPCDHTKGLECNFGASSTA 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                    SFRLYS 369
                                                                                                                                                                                                                                                                                                                              LSLPNLGCPNPRLV--KVSGQCCEEWVCDEDSIKDSLDDQDDLLGLDASEVE-----LTR 190
                                                                                                                                                                                                                                                                                                                                                                  CKCVCPADKQMSPGGCGS-----GKSFNKLTC--QCECDQSASKCGLKRWNADTCKCECQ
                                                                                                                                                                                                                                                                                                                                                                                                      LKGICRAQSEGRPCEYNSRIYQNGESFQP-NCKHQCTCIDGAVGC-----IPLCPQE 137
                                                                                                                                                                                                                                                                                                                                                                                                                                        CICPRDAPVCTAG----KERCGESCECKCINREPKEGCAKP-----LVWN----ENT 427
KQQIYN
                                                                         GQKWNDRVC-SC---GCPVP-----
                                                                                                            VKKYRPKYCGSCVDGRCCTPLQTRTVKMRFRCEDGEMFSKNVMMIQSCKCNYNCPHPNEA 363
                                                                                                                                                                                                                      KEKCKSPRQWTDSKCLCECSTTPATCEGKQTWCGEAC-----QCICPGGDKNCG---
                                                                                                                                                                                                                                                                                          PGMPPEGCGKQTWISDKCKCECSPTITCQAPQILD------LNTCECKCPVNMLAQ
                                                                                                                                                -NKKFFDKPSCECK-----CKNNPTCTSPQVWDADDCECKCPKDKQKPQ------GGCDG
                                                                                                                                                                                  STRVTNDNPECRLVKETRICEVRP-CGQP-VYSSLKKGKKCSKTKKSPEPVRFTYAGCSS
                                                                                                                                                                                                                                                        NNELIAIGKGSSLKRLPVFGTEPRVLFNPLHAHGQKCIVQTTSWSQC----SKSCGTGI 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
 676
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22.7%; Pred. No. 0.0
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                                                                         -RPDCTNGQIYN-----INTCACGCGIDKPSCP 670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .5; DB 2; 0.0057;
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Title:
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2103
    Query
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Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length DB
    CYR6_MOUSE
CYR6, EAT
NOV_HICK
NOV_CHICK
NOV_RAT
NOV_RAT
NOV_KENLA
CYR6_HUMAN
NOV_KENLA
CYR6_HUMAN
NOV_KENLA
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000622 homo sapien
P19336 gallus gall
Q9r1e9 rattus norv
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5 rattus norv
9 mus musculu
9 xenopus lae
4 mus musculu
1 homo sapien
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EMBL; M32490; AAA37512.1;
EMBL; X56790; CAA40109.1;
PIR; A35669; A35669.
MGD; MGI:88613; Cyr61.
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133.5	134	134	135	135.5	135.5	136	136.5	138	139	139.5	140	
6.3	6.4	6.4	6.4	6.4	6.4	6.5	6.5	6.6	6.6	6.6	6.7	
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P15270 dictyosteli	P54643 dictyosteli						Q02817 homo sapien					

ALIGNMENTS

RESULT	LT 1
	CYR6_MOUSE STANDARD; PRT; 379 AA.
DT AC	(Rel. 16,
DT	(Rel. 16,
Į Į	
	Cirbi protein precursor (Cysteine-rich, anglogenic inducer, bi) (Insulin-like growth factor-binding protein 10) (3CH61).
GN	CYR61 OR IGFBP10.
8	se).
88	hordata; Craniata; Vertebrata; Euteleosto
38	
RN	NCBL_18X1D=10090; [1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=BALB/c; TISSUE=Fibroblast;
RX	
RA	
RT	debe'."
	Mol. Cell. Biol. 10:3569-3577(1990).
D R	CHOTTENCE FROM N A
R :	STRAIN-AJ; TISSUE-Embryonic fibroblast;
RX	MEDLINE=91288203; PubMed=2062642;
RA A	a rout h
RI	immediate early gene cyr61.";
	Nucleic Acids Res. 19:3261-3267(1991).
	-!- FUNCTION: MAY ACT AS ONE OF THE MANY GROWTH FACTOR-BINDING
	PROTEINS; PROMOTES PROLIFERATION, MIGRATION AND ADHESTON.
ဂ	TISSUE SPECIFICITY: LOW IN KIDNEY, ADRENAL GLAND, TESTES, B
នន	AND OVARY, MODERATE IN HEART, UTERUS, AND SKELETAL MUSCLE, HIGHEST IN LUNG.
CC	STAGE: EXPRESSED FROM G(0)/G(1) THROUGH MID-G(1
88	NORMAL CELLS, AND AT
2 2	-i- INDUCTION: By growth factors. -i- SIMILARITY: Contains 1 IGFBP domain.
က	!- SIMILARITY: Contains
38	-!- SIMILARITY: Contains 1.TSP type-1 domain.
င္ပ	
음	SS-PROT entry is copyright. It is produced throug
	the European Bioinformatics Institute or Bioinformatics and the EMBL outstation .
	by non-profit institutions as long as its content is in no
	ed. Usage by and for commer
	entities requires a license agreement (see nttp://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).

20	EMRI: M32490: AAA37512 1

GO:0001569;

P:patterning

of blood vessels;

IMP

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RESULT
CYR6_RA
ID CY
AC Q9
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Best Local Sin
Matches 379;
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InterPro; IPR001007; VWF_C.
Pfam; PF00007; Cys_knot; 1.
Pfam; PF000219; IGFBP; 1.
Pfam; PF00090; tsp_1; 1.
Pfam; PF00090; tsp_1; 1.
SMART; SM00041; CT; 1.
SMART; SM00121; IB; 1
SMART; SM00121; IB; 1
CYR6_RAT
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InterPro; IPR006207; Cys_knot_C.
InterPro; IPR000867; Inst_gro_fac_pr.
InterPro; IPR000884; TSP1.
                                                                                                                     301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; SM00121; IB; 1.
; SM00209; TSP1; 1
; SM00214; VWC; 1.
TE; PS01185; CTCK
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                                                                                                                                                                CGTGISTRVTNDNPECRLVKETRICEVRPCGQPVYSSLKKGKKCSKTKKSPEPVRFTYAG
                                                                                                                                                                                        LDASEVELTRNNELIAIGKGSSLKRLPVFGTEPRVLFNPLHAHGQKCIVQTTSWSQCSKS
                                                                                                                                                                                                                                     CTCIDGAVGCIPLCPQELSLPNLGCPNPRLVKVSGQCCEEWVCDEDSIKDSLDDQDDLLG
                                                                                                                                                                                                                                                              NEDCSKTQPCDHTKGLECNFGASSTALKGICRAQSEGRPCEYNSRIYQNGESFQPNCKHQ
                                                                                                                                                                                                                                                                        NEDCSKTQPCDHTKGLECNFGASSTALKGICRAQSEGRPCEYNSRIYQNGESFQPNCKHQ
                                                                                                                                                                                                                                                                                               MSSSTERTLAVAVTLLHLTRLALSTCPAACHCPLEAPKCAPGVGLVRDGCGCCKVCAKQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PS01208; VWFC_1; PS50184; VWFC_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PS01225; CTCK_2; 1.
PS00222; IGF_BINDING;
PS50092; TSP1; 1.
                                                                                                                    CSSVKKYRPKYCGSCVDGRCCTPLQTRTVKMRFRCEDGEMFSKNVMMIQSCKCNYNCPHP
                                                                                                                             CSSVKKYRPKYCGSCVDGRCCTPLQTRTVKMRFRCEDGEMFSKNVMMIQSCKCNYNCPHP
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CYR61 PROTEIN.
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BY SIMILARITY.
BY SIMILARITY.
FA6B5014B56A8EE9 CRC64;
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           update)
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 update)
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5.6e-148;
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MSSSTERTLAVAVTLLHLTRLALSTCPAACHCPLEAPKCAPGVGLVRDGCGCCKVCAKQL

Matches

Conservative

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Indels

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Query Match
Best Local :
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PROSITE; PS01225; CTCK_2; 1.
PROSITE; PS00222; IGF_BINDING; 1
PROSITE; PS50092; TSP1; 1.
PROSITE; PS01208; VWFC_1; 1.
PROSITE; PS50184; VWFC_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- SUBCELLULAR LOCATION: S
-!- SIMILARITY: Contains 1
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-!- SIMILARITY: Contains 1
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                                            DOMAIN
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SMART;
SMART;
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Pfam; PF00093; vwc; 1
SMART; SM00041; CT; 1
SMART; SM00121; IB; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                        entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                              DOMAIN
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InterPro; IPR006207;
InterPro; IPR000867;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 modified and this statement is not removed. entitles requires a license agreement (See
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CYR61 protein precursor (Cysteine-rich, angiogenic inducer, (Insulin-like growth factor-binding protein 10).
                                                                                                                                                                                                                                                                                                                                      Pram;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=20435857;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CYR61 OR IGFBP10.
Local Sim
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Biol. Chem. 275:28929-28936(2000).
FUNCTION: MAY ACT AS ONE OF THE MANY GROWTH FACTOR-BINDING
PROTEINS; PROMOTES PROLIFERATION, MIGRATION AND ADHESION (1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           similarity)
                                                                                                                                                                                                                                                                                                                                     Pro; IPR001007; PF00007; Cys_k
                                                                                                                                                                                                                                                                   SM00209;
SM00214;
                                                                                                                                                                                       factor
           Similarity
                                           320
379
                                                                                                                                                                                                                                                                  ; IB; 1.
; TSP1; 1
: VWC; 1.
                                              ΑĄ,
                                                         oinding;
1 379
5 979
6 971
8 164
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2 351
3 353
353
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Contains 1 WMFC domain.

Contains 1 TSP type-1 domain.

Contains 1 C-terminal cystine knot-like (CTCK) domain.
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Der Kammer H., Ma
          98.98;
98.78;
                                              41687
                                                                                                                                                                                                                                                                                                                                                                      TSP1.
                                                                                                                                                                                                                                                                                                                                                                                           Cys_knot.
Cys_knot_C
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                                                                                                                                                                                       Signal
                                              WW;
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                                                        POTENTIAL.
CYR61 PROTEIN.
IGFBP.
TWFC.
TSP TYPE-1.
CTCK.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
 Pred. No. 3.30
2; Mismatches
             Score 2079;
Pred. No. 3
                                              62BF0BBA4C5AFDE9
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 es 3;
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                      Length
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RESULT
CYR6_H
                                                                         TISSUE-Placenta;
Kolesnikova T.V., Lau
Submitted (JUN-1997) t
                                                                                                                                                                                                                                                                                                                                                          CYR6_HUMAN STANDARD; PRT; 381 AA.

000622; 014934; 043775; Q9BZL7;

15-JUL-1998 (Rel. 36, Created)

15-JUL-1998 (Rel. 36, Last sequence update)

15-SEP-2003 (Rel. 42, Last annotation update)

CYR61 protein precursor (Cysteine-rich, angiogenic inducer,

CInsulin-like growth factor-binding protein 10) (GIG1 protein)
                                                                                                                           Martinerie C., Viegas-Pequignot E., "Chromosomal mapping and expression cells from the nervous system."; Mol. Pathol. 50:310-316(1997).
                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
  SEQUENCE FROM N.A.
Schuetze N., Lechner F
"Regulation of hCYR61
                                                                                                                                                                 SEQUENCE FROM N.A. MEDLINE-98197344;
                                                                                                                                                                                                                  "The
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                                                                                                                                                                                                                                                                                    SEQUENCE
Albrecht
                                                                                                                                                                                                                                                                                                                                                      CYR61 OR IGFBP10 OR GIG1.
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                                                                                                         SEQUENCE FROM N.A.
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14:1753-1757(1997)
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                                         (NOV-1997)
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            Koehrle
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AID DICTOR OCCORNATION OCCORNA

GO; GO:0008283; P:cell proliferation; GO; GO:0007345; P:embryogenesis and mc InterPro; IPR006208; Cys_knot_C. InterPro; IPR006207; Cys_knot_C. InterPro; IPR000867; Insl_gro_fac_pr. InterPro; IPR000867; Insl_gro_fac_pr. InterPro; IPR000867; VWF_C.

morphogenesis; TAS.

; PF00007; Cys_knot; ; PF00219; IGFBP; 1. ; PF00090; tsp_1; 1. ; PF00093; vwc; 1.

; VWF_C.

tsp_1; vwc; 1 ; CT; 1

EMBL; EMBL;

Genew;

BC016952; AAH16952; HGNC:2654; CYR61.

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RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Hopkins R.F., Jordan H., Moore T., Rabin G.M., Hong L.,
RA Hopkins R.F., Jordan H., Moore T., Rabin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunarathe P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Willalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Fahey J., Schein J.E., Jones S.J.M., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Blakesley R.W., T
                                                                                                                   EMBL;
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                                                                                                                                                                                                                                                                     EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EW the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entities requires a license agreement (See http://www.isb-sorsend an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY).

1. SUBCELLULAR LOCATION: Secreted.

1. SIMILARITY: Contains 1 IGFBP domain.

1. SIMILARITY: Contains 1 VWFC domain.

1. SIMILARITY: Contains 1 TSP type-1 domain.

1. SIMILARITY: Contains 1 C-terminal cystine knot-like (CTCK) domain.
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MEDLINE-22388257; PubMed-12477932;
Strausberg R.L., Feingold E.A., Gr
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Leng E., Tai G., Estable
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L; Y12084; CAA72802.1; -.
L; V13015; AAB58319.1; -.
L; Y11307; CAA72167.1; -.
L; Y11307; CAA72167.1; -.
L; AF003594; AAB61240.1; -.
L; AF031185; AAB84227.1; -.
L; AF031185; AAB84227.1; -.
L; AF031185; AAB84237.1; -.
L; AF031185; AAB84217.1; -.
L; AF031185; AAB84217.1; -.
L; BC001271; AAH01271.1; -.
L; BC001999; AAH16952.1; -.
L; BC001999; AAH16952.1; -.
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PROSITE; PS01225; CTCK_2; 1.

PROSITE; PS00222; IGF_BINDING; 1

PROSITE; PS50092; TSP1; 1.

PROSITE; PS01208; VWFC_1; 1.

PROSITE; PS50184; VWFC_2; 1.
                                                                                                                                                                                                                                                                                                CE10_CHICK
P19336;
01-NOV-1990
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15-SEP-2003
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                                                                                                              Eukaryota;
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NCBI_TaxID=9031;
                                                                           Archosauria;
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SM00209;
                                                                                                                                                protein precursor.
gallus (Chicken).
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                                                                        Metazoa; Chordata; (
a; Aves; Neognathae;
                                                                                                                                                                                                                        (Rel. 16, Created)
(Rel. 16, Last sequence up)
(Rel. 42, Last annotation
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                                                                                              Chordata;
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Pred. No. 8e-136;
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TSP TYPE-1.
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                                                                        Craniata; Vertebrata; Euteleostomi;
; Galliformes; Phasianidae; Phasianinae;
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PROSITE; PS50092; TSP1; 1.

PROSITE; PS50184; VWFC_1; 1.

PROSITE; PS50184; VWFC_2; 1.
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Pfam; PF00007; tsp_1; 1.
Pfam; PF00099; tsp_1; 1.
Pfam; PF00099; vwc; 1
SMART; SM00041; CT; 1
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SMART; SM00121; IB; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-89145206; PubMed-2537491;
Simmons D.L., Levy D.B., Yannoni Y., Erikson R.L.;
"Identification of a phorbol ester-repressible v-sr
Proc. Natl. Acad. Sci. U.S. A. 86:1178-1182(1989).
-!- FUNCTION: PROBABLE SECRETED REGULATORY PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           entities requires a license agreement (S or send an email to license@isb-sib.ch).
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-: SIMILARITY: Contains 1 IGFBP domain.
-: SIMILARITY: Contains 1 VWFC domain.
-: SIMILARITY: Contains 1 TSP type-1 domain.
-: SIMILARITY: Contains 1 C-terminal cystine knot-like (CTCK) domain.
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  EVELTRNNELIAIGKGSSLKRLPVFGTEP--RVLFNPLHAHGQKCIVQTTSWSQCSKSCG
                                                                   GCIPLCPQELSLPNLGCPNPRLYKVSGQCCEEWVCDEDSIKDSLDDQDDL----LGLDAS
                                                                                                                                                   PCDHTKGLECNEGASSTALKGICRAQSEGRPCEYNSRIYQNGESFQPNCKHQCTCIDGAV
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                                                                                                                                 PCDHTKGLECNFGASPAATNGICRAQSEGRPCEYNSKIYQNGESFQPNCKHQCTCIDGAV
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GTCK.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                      Score 1646.5;
Pred. No. 2.3e
Pred. Mismatches
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                                                                                                                                                                                                                                                                                                         2.3e-114;
hes 36;
                                                                                                                                                                                                                                                                                                                                                 DB
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Signal.

FACTOR

38;

Gaps

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THE RESULT CONTROL OF THE CONTROL OF
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28-FEB-2003 (Rel. 41, C
28-FEB-2003 (Rel. 41, L
28-FEB-2003 (Rel. 41, L
Connective tissue growt
                                            Pfam;
Pfam;
                                                                                                               InterPro;
InterPro;
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MEDILINE=20145935; PubMed=10679821;

MEDILINE=20145935; PubMed=10679821;

Xu J. Smcock S.L., Safadi F.F., Rosenzweig A.B.,

Xu J., Smcock S.L., Owen T.A., Popoff S.N.;

"Cloning the full-length cDNA for rat connective implications for skeletal development.";

J. Cell. Biochem. 77:103-115(2000).
                                                                                                                                                                                                                       EMBL; AF120275; AAD39132.1; -. EMBL; AB023068; BAA82125.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Rattus norvegicus connective tissue growth factor.";
Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
-i- FUNCTION: MAJOR CONNECTIVE TISSUE MITOATTRACTANT SECRETED
VASCULAR ENDOTHELIAL CELLS. PROMOTES PROLIFERATION AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Métazoa; Chordata;
Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10116;
                                                                                          Pfam;
                                                                                                                                                         InterPro;
                                                                                                                                                                                  InterPro;
                                                                                                                                                                                                       InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                   SYNTHESIS (D. CATTON: Secreted.
SUBCELULAR LOCATION: Secreted.
SIMILARITY: Contains 1 IGFBP domain.
SIMILARITY: Contains 1 VWFC domain.
SIMILARITY: Contains 1 TSP type-1 domain.
SIMILARITY: Contains 1 C-terminal cystine knot-like (CTCK) domain.
                                                                                                                                                                                                                                                                                                                                                                           SWISS-PROT entry is copyright. It is produced through a veen the Swiss Institute of Bioinformatics and the EMBL European Bioinformatics Institute. There are no restrict
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DIFFERENTIATION OF CHONDROCYTES (BY SIMILARITY). MEDIATES ADHESION AND ENHANCES FIBROBLAST GROWTH FACTOR-INDUCED DNA SYNTHESIS (BY SIMILARITY).
                                            PF00219;
PF00090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         363
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                                                                                   Pro; IPR006207; Cys_knot_C.
Pro; IPR000867; Insl_gro_fac_pr.
Pro; IPR001884; TSP1.
Pro; IPR001007; WWF_C.
PP00007; Cys_knot; 1.
                                                                                                                                                                                                                                                                                      non-profit institutions as long as its content is in no way d and this statement is not removed. Usage by and for commercial s requires a license agreement (See http://www.isb-sib.ch/announce/an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A-YPFYRLVNDIHKFRD
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  IGFBP;
tsp_1;
vwc; 1.
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41, Last annotation updat
growth factor precursor.
                                                                                                                                                                                                     Cys_knot.
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  RESULT 6
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Matches 176
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PROSITE; PS01185; CTCK_2; 1.

PROSITE; PS01225; CTCK_2; 1.

PROSITE; PS00222; IGF_BINDING; 1

PROSITE; PS00222; IGF_BINDING; 1

PROSITE; PS01208; VWFC_1; 3.

R PROSITE; PS011208; VWFC_1; 3.

R PROSITE; PS01184; VWFC_2; 3.

R PROSITE; PS01185; PS011
                                                                                                      OTGF_MOUSE STANDARD; PRT; 348 AA. P. 729268; 092200; 01-DEC-1992 (Rel. 24, Created) 28-FEB-2003 (Rel. 41, Last sequence update) 15-SEP-2003 (Rel. 42, Last annotation update) Connective tissue growth factor precursor (FISP-12 (Hypertrophic chondrocyte-specific protein 24). CTGF OR FISP12 OR FISP-12 OR HCS24.
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SMART;
SMART;
                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
NCBI_TaxID=10090;
                                                                                     Mus musculus (Mouse)
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SM00214; VWC; 1
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Pred. No. 7.5e
61; Mismatches
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CTCK.
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A -> R (IN REF.
T -> P (IN REF.
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P (IN REF. 2)
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                                            Muridae;
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Euteleostomi;

Murinae;

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RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Willalon D.K., Muzny D.M., Sodergren E.J., Lu X., Glibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Butkesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Butkesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Butterfield Y.S.N., Krzywinski M.I., Schalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.",
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                  DIFFERENTIATION OF CHONDROCYTES (BY SIMILARITY). MEDIATES CELL
ADHESION AND ENHANCES FIBROBLAST GROWTH FACTOR-INDUCED DNA
SYNTHESIS (BY SIMILARITY).

-!- SUBUNIT: MONOMEY (BY SIMILARITY).

-!- TISSUE SPECIFICITY: TESTIS, SPLEEN, KIDNEY, LUNG, HEART, AND BRAIN
(LOWEST LEVEL IN TESTIS AND HIGHEST IN LUNG).

-!- INDUCTION: BY GROWTH FACTORS.

-!- SIMILARITY: Contains 1 IGFBP domain.

-!- SIMILARITY: Contains 1 TSP type-1 domain.

-!- SIMILARITY: Contains 1 C-terminal cystine knot-like (CTCK) domain.
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"Fispl2/mouse connective tissue growth factor mediates endothelial cell adhesion and migration through integrin alphavbeta3, promotes endothelial cell survival, and induces angiogenesis in vivo.";
Mol. Cell. Biol. 19:2958-2966(1999).
                                                                                                                                                                                                                                                                                                                     This
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"Cyr61 and Fispl2 are both ECM-associated signaling
"Cyr61 and Fispl2 are both Towally attended the deve
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Brunner A., Chinn J., Neubauer M.G.,
"Identification of a gene family reg
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                                                                     entry is copyright. It is produced through a collaboration iss Institute of Bioinformatics and the EMBL outstation solutions in the control of the control o
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SMART; SM00209; TSP1; 1
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GO: GO:0008201;

GO: GO:0005178;

GO: GO:0001525;

GO: GO:00016477;

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or send a
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PROSITE; PS01225; CTCK_2; 1.
PROSITE; PS00222; IGF_BINDING;
PROSITE; PS50092; TSP1; 1.
PROSITE; PS01208; VWFC_1; 1.
PROSITE; PS50184; VWFC_2; 1.
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 CSKSCGTGISTRVTNDNPECRLVKETRICEVRPCGQPVYSSLKKGKKCSKTKKSPEPVRF
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C:extracellular matrix; IDA.
F:heparin binding activity;
F:integrin binding activity;
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TSP TYPE-1.
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                                                                                                                                                                                                  957.5;
No. 1.
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                                                                                                                                                                                                                                                                                                                                                   TISSUE
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296
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267

297 208

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CTGF_HUMAN
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                                                                                                                            TISSUE-Chondrocytes;

MEDLINE-20080284; PubMed-10614647;

Nakanishi T., Nishida T., Shimo T., Kobayashi K., Kubo T..

Tamatani T., Tezuka K., Takigawa M.;

"Effects of CTGF/HCs24, a product of a hypertrophic chond:ocyte-
specific gene, on the proliferation and differentiation of
chondrocytes in culture.";

Endocrinology 141:264-273(2000).

-i- FUNCTION: MAJOR CONNECTIVE TISSUE MITOATTRACTANT SECRITED BY
VASCULAR ENDOTHELIAL CELLS. PROMOTES PROLIFERATION AND
DIFFERENTIATION OF CHONDROCYTES. MEDIATES CELL ADHESION AND
ENHANCES FIBROBLAST GROWTH FACTOR-INDUCED DNA SYNTHESIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Marz W., Rupp J., Pech M., Luescher T.F.;
"Human connective tissue growth factor is expratherosclerotic lesions.";
Circulation 95:831-839(1997).
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P29279; Q96QX2;
01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Connective tissue growth factor precursor (Hypertrophic chondrocyte-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE-Umbilical vein endothelial cell MEDLINE-93187114; PubMed-1293144; Igarashi A., Bradham D.M., Okochi H., "Connective tissue growth factor."; J. Dermatol. 19:642-643(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bradham D.M., Igarashi A., Potter R.L., Grotendorst G.R.;
"Connective tissue growth factor: a cysteine-rich mitogen secreted human vascular endothelial cells is related to the SRC-induced immediate early gene product CEF-10.";
J. Cell Biol. 114:1285-1294(1991).
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Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutelnostomi;
Mammalia: Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     specific protein 24).
CTGF OR HCS24.
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Oemar B.S., Werner A., Garnier J.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=91373462; PubMed=1654338;
Bradham D.M., Igarashi A., Potter
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TISSUE-Umbilical vein
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                       SUBUNIT: MONOMER SUBCELLULAR LOCATION: FOUND IN SOLUBLE FORM (BY SIMILARITY) ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         357
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splicing; Named isoforms=2;
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                                                                                     EXTRACELLULAR
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Matches

64;

Indels

48;

Gaps

9;

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Query Match
Best Local
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Pfam; PF00093; vwc; 1.
SMART; SM00041; CT; 1.
SMART; SM00121; IB; 1.
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                                        CONFLICT
                                                                                                                                                                    DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                         GO; GO:0005578; C:extracellular matrix; TAS.
GO; GO:0005886; C:plasma membrane; TAS.
GO; GO:0005520; F:insulin-like growth factor bindi
GO; GO:0008151; P:cell growth and/or maintenance;
GO; GO:0008544; P:epidermal differentiation; TAS.
GO; GO:0008611; P:response to wounding; TAS.
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                                                                                                                                               DISULFID
                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                            SIGNAL
                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00007; Cys_knot; Pfam; PF00219; IGFBP; 1.
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                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                      Alternative
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                                                                                                                                                                                                                                           PROSITE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY: Contains 1 TSP type-1 domain.
SIMILARITY: Contains 1 C-terminal cystine knot-like (CTCK)
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al Similarity
176; Conserv
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                                                                                                                                                                                                                                                                                                       SM00214; VWC; 1
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                                                                                                                                                                                                                                                                                                                SM00209; TSP1;
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                                                                                                                                                                                                                                         PS50184;
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IPR001007;
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                                      83
349
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IGF_BINDING;
ISP1; 1.
VWFC_1; 1.
VWFC_2; 1.
                                                                                                                                                                                                                                                                                             CTCK_1;
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                                                                        synthesis;
                                        83
38069
        45.2%;
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BY SIMILARITY.

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N-LINKED (GLCNAC...

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        Score 950;
Pred. No. 4.
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                                       /FTId=VSP_002460.
D -> H (IN REF. 4)
0ECF8470B357EA95
                                                                                                                                                                   VWFC.
TSP TYPE-1.
                                                                                                                                                                                      IGFBP.
                                                                                                                                                                                                  CONNECTIVE
                                                                                                                                                                                                                                Extracellular matrix;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                factor binding activity; TAS maintenance; TAS.
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                                                                                                                                                                                                  TISSUE
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                    DB 1;
        1e-63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 as its content.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           http://www.isb-sib.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Usage
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                  Length 349;
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                                                                                                                                                                                                                                Signal;
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RESULT CONTROL OF THE                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       밁
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15-UUL-1998 (Rel. 36, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Connective tissue growth factor precursor.
                    between
the Euro
                                                                                                                                                                                                                                                                             chromosomal gene and demonstration of promoter activity."; Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
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018739; Q96
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Kanitz M., Kauffmann
Submitted (AUG-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bos taurus (Bovine).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea

Bovidae; Bovinae; Bos.

NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                      Mathahs M., Schwitters C., Hove M., Rupp "Bovine connective tissue growth factor,
                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Liver;
                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                       DIFFERENTIATION OF CHONDROCYTES (BY SIMILARITY). MEDIATES CELL ADHESION AND ENHANCES FIBROBLAST GROWTH FACTOR-INDUCED DNA SYNTHESIS (BY SIMILARITY).

SUBBUNIT: Monomer (By similarity).

SUBCELULIAR LOCATION: FOUND IN THE EXTRACELLULAR MATRIX AND AS A SOLUBLE FORM (BY SIMILARITY).

SIMILARITY: Contains 1 IGFBP domain.

SIMILARITY: Contains 1 TSP type-1 domain.

SIMILARITY: Contains 1 TSP type-1 domain.

SIMILARITY: Contains 1 C-terminal cystine knot-like (CTCK) domain.
                    s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                FUNCTION: MAJOR CONNECTIVE TISSUE MITOATTRACTANT SECRETED VASCULAR ENDOTHELIAL CELLS. PROMOTES PROLIFERATION AND
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|:|||||| | |::||::|||::||::|||::|||
CRVCAKQLGELCTERDPCDPHKGLFCDFGSPANRKIGVCTAK-DGAPCIFGGTVYRSGES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TEWSACSKTCGMGISTRVTNDNASCRLEKQSRLCMVRPCEADLEENIKKGKKCIRTPKIS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MSSSTERTLAVAVTLLHLTRLALSTCPAA------CHCPLE-APKCAPGVGLVRDGCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FQPNCKHQCTCIDGAVGCIPLCPQELSLPNLGCPNPRLVKVSGQCCEEWVCDEDSIKDSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MTAASMGPVRVAFVVL----LALCSRPAVGQNCSGPCRCPDEPAPRCPAGVSLVLDGCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;

    Fotsis T., Schimanski M., Bierhaus A.,
nn G., Schweigerer L., Ziegler R., Nawroth
    to the EMBL/GenBank/DDBJ databases.

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Best Local
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PROSITE; PS01225; CTCK_2; 1.
PROSITE; PS01225; IGE_BINDING; 1
PROSITE; PS50092; TSP1; 1.
PROSITE; PS01208; VMFC_1; 1.
PROSITE; PS01208; VMFC_1; 1.
Cell adhesion; DNA synthesis; Ex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR006207; Cys_knot
InterPro; IPR000847; Insl_gro
InterPro; IPR000884; TSP1.
InterPro; IPR001007; VWF_C.
Pfam; PF00007; Cys_knot; 1.
Pfam; PF000219; IGFBP; 1.
Pfam; PF000219; tSFBP; 1.
Pfam; PF00093; vwc; 1.
SMART; SM00041; CT; 1.
SMART; SM00041; CT; 1.
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CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     entities requires a license agreement (S or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
   EPVRFTYAGCSSVKKYRPKYCGSCVDGRCCTPLQTRTVKMRFRCEDGEMFSKNVMMIQSC
                                  TEWSACSKTCGMGISTRVTNDNAFCRLEKQSRLCMVRPCEADLEENIKKGKKCIRTPKIS
                                                      TSWSQCSKSCGTGISTRVTNDNPECRLVKETRICEVRPCGQPVYSSLKKGKKCSKTKKSP
                                                                                                                                                                                             CKYCAKQLNEDCSKTQPCDHTKGLECNFGASSTALKGICRAQSEGRPCEYNSRIYQNGES
                                                                                                                                                                                                                                                                                                                                                      MSSSTFRTLAVAVTLLHLTRLALST-----CPAACHCPL-EAPKCAPGVGLVRDGCGC
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                                                                                                                                        DDQDDLLGLDASEVELTRNNELIAIGKG-SSLKRLPVFGTEPRVLFNPLHAHGQKCIVQT
                                                                                                                                                                         FQSSCKYQCTCLDGSVGCVPLCSVDVRLPSPDCPFPRRVKLPGKCCEEWVCDEP-----
                                                                                                                                                                                                                                                                                                                     MSATGLGPVRCAFVLL----LALCSRPASSQDCSAPCQCPAGPAPRCPAGVSLVLDGCGC
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37924 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Cys_knot.
; Cys_knot_C.
; Insl_gro_fac_pr.
; Tsp1.
                                                                                                                                                                                                                                                                                                                                                                                                           44.68;
44.78;
                                                                                                                                                                                                                                                                                                                                                                                          65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TSP TYPE-1.

CTCX.

BY SIMILARITY.

L -> DC (IN REF. 1).

CDEP -> SRDE (IN REF. 1).

CDEP -> C (IN REF. 1).

C -> F (IN REF. 1).

C -> F (IN REF. 1).

C -> F (IN REF. 1).
                                                                                                       -KEHTVVGPALAAYRPEDTFGPDPTMI - - -
                                                                                                                                                                                                                                                                                                                                                                                       Score 937; DB Pred. No. 3.7e 55; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POTENTIAL.
CONNECTIVE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE GROWTH FACTOR
                                                                                                                                                                                                                                                                                                                                                                                                           DB 1;
.7e-62;
                                                                                                                                                                                                                                                                                                                                                                                            100;
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Signal.

Indels

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Gaps

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- RANCLVQT

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15-JUL-1998 (Rel. 3
15-JUL-1998 (Rel. 3
28-FEB-2003 (Rel. 4
                                               PROSITE;
PROSITE;
PROSITE;
                                                                                                                                                                              InterPro; IPR006208; Cys_knot.
InterPro; IPR006207; Cys_knot_C.
InterPro; IPR000867; Insl_gro_fac_pr.
InterPro; IPR000884; TSP1.
InterPro; IPR001007; VWF_C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      _PIG
LT 9
                                                                                                  SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sus scrofa (Pig).
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                    use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                 This
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                                                                                     SMART;
                                                                                                                         SMART;
                                                                                                                                                   Pfam;
                                                                                                                                                               Pfam;
                                                                                                                                                                          Pfam;
                                                                                                                                                                                                                                                   EMBL; U83916; AAC48756.1;
                                                                                                                                                                                                                                                                       entities requires a license agreement (See http://www.ish-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                          the
                                                                                                                                                                                                                                                                                                                                     between
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Purification and characterization of novel heparin-binding factors in uterine secretory fluids. Identification as hepar regulated Mr 10,000 forms of connective tissue growth factor J. Biol. Chem. 272:20275-20282(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Brigstock D.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=97390475;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9823;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BIO1. Chem. 272:20275-20282(1997).
FUNCTION: MAJOR CONNECTIVE TISSUE MITOATTRACTANT SECRET VASCULAR ENDOTHELIAL CELLS. PROMOTES PROLIFERATION AND DIFFERENTIATION OF CHONDROCYTES (BY SIMILARITY). MEDIAN ADHESION AND ENHANCES FIBROBLAST GROWTH FACTOR-INDUCED
                                                                                 m; PF00007; Cys_knot; 1.
m; PF00007; Cys_knot; 1.
m; PF00090; tsp_1; 1.
m; PF000903; vwc; 1.
kT; SM00041; CT; 1.
kT; SM00121; IB; 1.
kT; SM00210; TSP1; 1.
kT; SM00214; VWC; 1.
                                                                                                                                                                                                                                                                                                                        ween the
European
                                                                                                                                                                                                                                                                                                                                                                   SUBUNIT: MONOMER (By similarity).

SUBCELLULAR LOCATION: FOUND IN THE EXTRACELLULAR MATRIX AND AS A SOLUBLE FORM (BY SIMILARITY).

SIMILARITY: Contains 1 IGFBP domain.

SIMILARITY: Contains 1 VWFC domain.

SIMILARITY: Contains 1 TSP type-1 domain.

SIMILARITY: Contains 1 C-terminal cystine knot-like (CTCK) domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             SYNTHESIS
                                                                                                                                                                                                                                                                                                                      SWISS-PROT entry is copyright. It is produced through
een the Swiss Institute of Bioinformatics and the EN
European Bioinformatics Institute. There are no resti
 adhesion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      324
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       3; PS01185; CTCK_1; 1.
3; PS01225; CTCK_2; 1.
8; PS00222; ITSP; 1.
8; PS50092; TSP; 1.
8; PS01208; VWFC_1; 1.
8; PS01208; VWFC_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P.A.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                             (BY SIMILARITY)
 DNA synthesis;
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teffen C.L., Kim
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41, Last annotation update)
growth factor precursor.
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Extracellular matrix; Signal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    G.Y.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local S
Matches 173
                                                                                                                                                                                                            P28686;
01-DEC-1992 (Rel. 2
01-DEC-1992 (Rel. 2
28-FEB-2003 (Rel. 4
nephroblastomas.";

MO1. Cell. Biol. 12:10-21(1992).

MO1. Cell. Biol. 12:10-21(1992).

-!- FUNCTION: IMMEDIATE-EARLY PROTEIN LIKELY TO PLAY A ROLE GROWTH REGULATION. ITS OVEREXPRESSION IS ASSOCIATED WIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
DOMAIN
DOMAIN
DISULFID
DISULFID
DISULFID
DISULFID
                                                                                  STRAIN-Brown leghorn;
MEDLINE-92107157; PubMed=1309586;
Joliot V., Martinerie C., Dambrin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIGNAL CHAIN
                                                                                                                                                                   Gallus gallus (Chicken)
Finharvota; Metazoa; Chordata;
                                                      Crochet J., Perbal B.;
"Proviral rearrangements and overexpression of (nov) in myeloblastosis-associated virus type
                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                          Archosauria;
                                                                                                                                                           Eukaryota; Metazoa;
Archosauria; Aves; 1
                                                                                                                              NCBI_TaxID=9031;
[1]
                                                                                                                                                                                                                                                    NOV_CHICK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
les 173; Conserv
                                                                                                                                                                                                  protein
                                                                                                                                                                                                                                                                                                      324
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                                                                                                                                                                                                                                                                                                                                                                                               TSWSQCSKSCGTGISTRVTNDNPECRLVKETRICEVRPCGQPVYSSLKKGKKCSKTKKSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CKYCAKQLNEDCSKTQPCDHTKGLECNFGASSTALKGICRAQSEGRPCEYNSRIYQNGES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MSSSTERTLAVAVTLLHLTRLALSTCPAA-----CHCPL-EAPKCAPGVGLVRDGCGC
                                                                                                                                                                                                                                                                                                      ACHYNCPGDNDIFESLYYRKMYGDM
                                                                                                                                                                                                                                                                                                                         KCNYNCPHPNEASFRLY - - SLFNDI
                                                                                                                                                                                                                                                                                                                                            DDQDDLLGLDASEVELTRNNELIAIGKGSSLKRL-PVFGTEPRVLFNPLHAHGQKCIVQT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FQPNCKHQCTCIDGAVGCIPLCPQELSLPNLGCPNPRLVKVSGQCCEEWVCDEDSIKDSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CRLCAKQLGELCTERDPCDPHKGLFCDFGSPANRKIGVCTAK-DGAPCVFGGTVYRSGES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MSATGLSPVRCAFVLL----LALCSRPASGQDCSGQCQCAAGKRRACPAGVSLVLDGCGC
                                                                                                                                                                                                                                                                                                                                                               EPVRFTYAGCSSVKKYRPKYCGSCVDGRCCTPLQTRTVKMRFRCEDGEMFSKNVMMIQSC
                                                                                                                                                                                                                                                                                                                                                                                     TEWSACSKTCGMGISTRVTNDNAFCRLEKOSRLCMVRPCEADLEENIKKGKKCIRTPKIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FQSSCKYQCTCLDGAVGCVPLCSMDVRLPSPDCPFPRRVKLPGKCCEEWVCDEP--KDH-
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                                                                                                                                                                                                                                                     STANDARD;
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349
1100
1167
243
-330
293
307
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24,
                                                                                                                                                           Neognathae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    43.78;
                                                                                                                                                                                                  Last sequence up
Last annotation
(Nephroblastoma
                                                                                                                                                                                                                                Created)
                                                                                                                                                                                                                                                                                                                                                                                                                             ----TVVGPALAAYRLEDTFGPDPTMM-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  W.
                                                                                      Dambrine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TSP TYPE-1.
CTCK.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 919; DB Pred. No. 7.9e 32; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IGFBP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL.
CONNECTIVE
                                                                                                                                                           Craniata; Vertebrata; Euteleostomi;
; Galliformes; Phasianidae; Phasiani
                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BB510E2B2B52D4A0
                                                                                     G.,
                                                                                                                                                                                                                                                                                                                         374
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overexpressed
                                                                                      Plassiart
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                                                        a new cellular
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                                                                                     G.,
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                                                                                                                                                                                                  gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FACTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               349;
                                                                                                                                                           Phasianinae;
                                                                                                                                                                                                   protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           48;
                                                                                                                                                                                                                                                                                                                                                                                                                             -RANCLVQT
                                                                 gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    172
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                                                                                                                        Query Match
                                                                                                                                                                                                                                                              SMART; SM00209; TSP1; 1.

SMART; SM00211; VWC; 1.

PROSITE; PS001185; CTCK_1; 1.

PROSITE; PS01225; CTCK_2; 1.

PROSITE; PS00222; IGF_HINDING; 1

PROSITE; PS00092; TSP1; 1.

PROSITE; PS01208; VWFC_1; 1.

PROSITE; PS011084; VWFC_2; 1.
                                                                                                                                                  DISULFID
DISULFID
DISULFID
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DISULFID
CARBOHYD
                                                                                                                                                                                                             DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                              Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWI
                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                        CHAIN
                                                                                                                                                                                                                                                SIGNAL
                                                                                                                                                                                                                                                                                                                                            SMART;
                                                                                                                                                                                                                                                                                                                                                              Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                          SEQUENCE
                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the
                                                                                                                                                                                                                                                        Proto-oncogene;
                                                                                                                                                                                                                                                                                                                                                                       Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                 PIR; S20078;
                                                                                                                                                                                                                                                                                                                                    SMART;
                                                                                                                                                                                                                                                                                                                                                      Pfam;
                                                                                                                                                                                                                                                                                                                                                                                        InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                       interPro;
                                                                                                                 Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY: Contains 1 IGFBP domain.
SIMILARITY: Contains 1 VWFC domain.
SIMILARITY: Contains 1 TSP type-1 domain.
SIMILARITY: Contains 1 C-terminal cystine knot-like (CTCK) domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MUSCLE AND INTESTINE, IN THE EMBRYO. I SPLEEN, IN THE EMBRYO. I SPLEEN, IN ADULT CHICKEN.
DEVELOPMENTAL STAGE: MAVI-INDUCED NEPH LEVEL OF NOV GENE WHOSE TRANSCRIPTION ADULT KIDNEY.
                                                                                                                                                                                                                                                                                                                                 1; PF00007; Cys_knot; 1.
1; PF000219; IGFBP; 1.
1; PF000909; tsp_1; 1.
1; PF00093; vwc; 1.
2T; SM00041; CT; 1.
2T; SM00021; IB; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBCELLULAR LOCATION: Secreted TISSUE SPECIFICITY: BRAIN AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P G
128
                 122
                                                                                                        165;
                                   69
                                                                                                                                                                                                                                                                                                                                                                                                                                         X59284;
                                                   62
                                                                     9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NOV GENE IN CHICKEN EMBRYONIC FIBROBLASTS (CEF) INDUCE THE TRANSFORMATION OF CEF IN VITRO.
                                                                                                                Similarity
TCRDGQIGCLPRCNLGLLLPGPDCPFPRKIEVPGECCEKWVCDPRDEVLLGGFAMAAYRQ
               TCIDGAVGCIPLCPQELSLPNLGCPNPRLVKVSGQCCEEWVCD-EDSI-----KDSLDDQ
                                           EDCSKTQPCDHTKGLECNFGASSTALKGICRAQSEGRPCEYNSRIYQNGESFQPNCKHQC
                                                                             LAVAVTLLHLTRLA-----LSTCPAAC--HCPLEAPKCAPGVGLVRDGCGCCKVCAKQLN
                                ESCSPLLPCDESGGLYCDRGPEDGGGAGICMV-LEGDNCVFDGMIYRNGETFQPSCKYQC
                                                                    LPVLLLLLLLRPCEVSGREAACPRPCGGRCPAEPPRCAPGVPAVLDGCGCCLVCARQRG
                                                                                                                                                                                                                                                                                                                                                                                                               IPR006208;
IPR006207;
                                                                                                                                                                                                                                                                                                                                                                                       IPR001007;
                                                                                                                                                                                                                                                                                                                                                                                               IPR000867;
IPR000884;
                                                                                                                                         31
104
201
258
258
275
286
289
294
                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                  S20078.
                                                                                                                                                                                                                                                                                                                                                                                                                                           CAA41975.1;
                                                                                                                                          AA;
                                                                                                                                                                                                                                                        Growth
                                                                                                                                                           351
103
170
246
246
332
395
309
325
331
                                                                                                                                                                                                                                                                                                                                                                                              ; Cys_knot.
; Cys_knot_C.
; Insl_gro_fac_pr.
; TSP1.
                                                                                                               40.98;
                                                                                                                                         38268
                                                                                                                                                                                                                                                                                                                                                                                     VWF_C.
                                                                                                                                                                                                                                                        factor;
                                                                                                                                         MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Secreted.
                                                                                                        44;
                                                                                                                                                CTCK.
BY SIMILARITY.
                                                                                                   Pred. NO. 1.35
                                                                                                                                                                                                            VWFC.
TSP TYPE-1.
                                                                                                                      Score 861;
                                                                                                                                                                                                                                      VOV
                                                                                                                                                                                                                              IGFBP.
                                                                                                                                                                                                                                                       Signal.
                                                                                                                                         1ECB3FA3058C6797
                                                                                                                                                                                                                                     PROTEIN
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                                                                                                                5e-56
                                                                                                                        DB 1;
                                                                                                        110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Usage
                                                                                                                     Length
                                                                                                                                         CRC64;
                                                                                                       Indels
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LESS 9
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SO IN B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUFFICIENT
                                                                                                       52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BRAIN AND
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                                                                                                      Gaps
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187
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       PROSITE;
PROSITE;
PROSITE;
Proto-oncogene;
                                                                                                                                                                                                                                                                                                                                                                                                       VOV
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RESULT 11
NOV_COTJA
                                                                                                                Pfam; PF00219; IGFBP; 1
Pfam; PF00090; tsp_1; 1
Pfam; PF00093; vwc; 1.
SMART; SM00041; CT; 1.
SMART; SM00121; IB; 1.
SMART; SM00209; TSP1; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NOV_COTJA
P42642;
01-NOV-1995
01-NOV-1995
28-FEB-2003
                                                    SMART; SM
PROSITE;
PROSITE;
PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
Weiskirchen R., Bister K.;
Weiskirchen R., Bister K.;
Submitted (AUG-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        This
                                                                                                                                                                                                                                                                                                                                                                                          use by non-profit institutions as long modified and this statement is not removed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GROWTH REGULATION (BY SIMILARITY).

-!- SUBCELLULAR LOCATION: Secreted (By similarity).

-!- SIMILARITY: Contains 1 IGFBP domain.

-!- SIMILARITY: Contains 1 VWFC domain.

-!- SIMILARITY: Contains 1 TSP type-1 domain.

-!- SIMILARITY: Contains 1 C-terminal cystine knot-like (CTCK) domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Coturnix coturnix japonica (Japanese quail).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                          Pfam;
                                                                                                                                                                                                                                          InterPro; IPR001007;
                                                                                                                                                                                                                                                                                                                         EMBL; U13063; AAA21128.1; -
                                                                                                                                                                                                                                                                                                                                                       entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                          between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Coturnix
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NOV protein
                                                                                                                                                                                                                                                       InterPro;
                                                                                                                                                                                                                                                                           InterPro;
                                                                                                                                                                                                                                                                                        InterPro;
                                                                                                                                                                                                                                                                                                            InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                         European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                     SWISS-PROT entry is copyright. It is produced through
een the Swiss Institute of Bioinformatics and the El
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               176
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E; PS01185; CTCK_1; 1.
E; PS01225; CTCK_2; 1.
E; PS00222; IGF_BINDING; 1
E; PS50092; TSP1; 1.
3; PS01208; VWFC_1; 1.
3; PS50184; VWFC_2; 1.
                                                                                                                                                                                                                          PF00007;
                                                                                                        SM00214;
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                                                                                                                                                                                                                                                       IPR006208; Cys_knot.
IPR006207; Cys_knot_C.
IPR000867; Insl_gro_fac_pr.
IPR000884; TSP1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (Rel. 32, Created)
(Rel. 32, Last sequence up
(Rel. 41, Last annotation
precursor (Nephroblastoma
                                                                                                                                                                                                                       Cys_knot;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                        VWC;
                                                                                                                                                                                                                                                                                                                                                                          license agreement
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RA Klausner R.D., Feligold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Raha S.S., WoEban P.J., McKernan K.J., Malek J.A., Gunaratree P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RGeneration and initial analysis of more than 15,000 full-length
A.T. Munan and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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"The C-terminal domain of the regulatory protein NOVH is
promote interaction with fibulin IC: a clue for a role of
cell-adhesion signaling.";
Proc. Natl. Acad. Sci. U.S.A. 96:869-874(1999).
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Best Local :
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SMART; SM00209; TSP1; 1.
SMART; SM00214; VWC; 1.
PROSITE; PS01185; CTCK_1; 1.
PROSITE; PS01225; CTCK_2; 1.
PROSITE; PS00222; IGF_BINDING; 1
PROSITE; PS00022; TSP1; 1.
PROSITE; PS01008; VWFC_1; 1.
PROSITE; PS011008; VWFC_2; 1.
                                                                                                                Q9QZQ5;
28-FEB-2003
28-FEB-2003
15-SEP-2003
NOV protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DISULFID
DISULFID
CARBOHYD
CARBOHYD
CONFLICT
SEQUENCE
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                  Eukaryota; Metazoa;
Mammalia; Eutheria;
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DOMAIN
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                                                                                                gene protein
                                                             Rattus norvegicus
                                                                                                                                                                                                                   NOV_RAT
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  NCBI_TaxID=10116;
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                                                                                                                                                                                                                                                                                                                                                                                                 272
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FQPNCKHQCTCIDGAVGCIPLCPQELSLPNLGCPNPRLVKVSGQCCEEWVCDEDSIKDSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLYCARQRGESCSDLEPCDESSGLYCDRSADPSNQTGICTA-VEGDNCVEDGVIYRSGEK
                                                                                                                                                                                                                                                                                                                   TCHTNCPKNNEA
                                                                                                                                                                                                                                                                                                                                            KCNYNCPHPNEA
                                                                                                                                                                                                                                                                                                                                                                                               KAIHLQFKNCTSLHTYKPRFCGVCSDGRCCTPHNTKTIQAEFQCSPGQIVKKPVMVIGTC
                                                                                                                                                                                                                                                                                                                                                                                                                      EPVRFTYAGCSSVKKYRPKYCGSCVDGRCCTPLQTRTVKMRFRCEDGEMFSKNVMMIQSC
: : |:|: |:| |:| :| :| :|
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SWSQCSKSCGTGISTRYTNDNPECRLYKETRICEVRPCGQ-PYYSSLKKGKKCSKTKKSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GG----SDSSV-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FQPSCKFQCTCRDGQIGCVPRCQLDVLLPEPNCPAPRKVEVPGECCEKWICGPDE-EDSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CKVCAKQLNEDCSKTQPCDHTKGLECNFGASSTALKGICRAQSEGRPCEYNSRIYQNGES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VQSTSFCLRKQCLCLTFLLLHLLGQVAATQRCPPQCPGRCPATPPTCAPGVRAVLDGCSC
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                                                                                                                                   (Rel. 41, Created)
(Rel. 41, Last sequence up
(Rel. 42, Last annotation
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108
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                                                                                                homolog).
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29162
                                                         (Rat)
                  Chordata;
Rodentia;
                                                                                                                    precursor (NovH) (Nephroblastoma
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TSP TYPE-1.
CTCX.
BY SIMILARITY.
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BY SIMILARITY.
OF SIMILARITY.
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N-LINKED (GLCNAC...) (1
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Pred. No. 5.
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                Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IGFBP.
                                                                                                                                                                                                                       PRT;
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                                                                                                                                         update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           116;
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                                                                                                                  overexpressed
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                    Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          172
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                                                                                                      Query Match
Best Local
                                                              Matches
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Pfam; PF00093; vwc; 1.
SMART; SM00041; CT; 11;
SMART; SM00121; IB; 1.
SMART; SM00209; TSP1;
SMART; SM00214; VWC; 1
                                                                                                               CARBOHYD
CARBOHYD
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Growth fa
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DOMAIN
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PROSITE; PS00222; IGF_BINDING;
PROSITE; PS50092; TSP1; 1.
PROSITE; PS01208; VWFC_1; 1.
PROSITE; PS50184; VWFC_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- TISSUE SPECIFICITY: Ubiquitous.
-!- SIMILARITY: Contains 1 IGFBP domain.
-!- SIMILARITY: Contains 1 VWEC domain.
-!- SIMILARITY: Contains 1 TSP type-1 domain.
-!- SIMILARITY: Contains 1 C-terminal cystine knot-like (CTCK)
                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                       SIGNAL
                                                                                                                                                                                                                                                                                                            PROSITE; PS01185;
                                                                                                                                                                                                                                                                                                                                                                                   Pfam;
                                                                                                                                                                                                                                                                                                                                                                                             Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AF171936;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     modified and this statement is not removed. entities requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Liu C., Liu X.J., Crowe P.D., Keln-
Ling N., De Souza E.B., Maki R.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            [1]
SEQUENCE FROM N.A., AND CHARACTERI
STRAIN-Sprague-Dawley;
MEDLINE-20035752; PubMed-10570975;
                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                       InterPro;
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                                                                      Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein.
SUBUNIT: Interacts with SUBCELLULAR LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FUNCTION: Can act specific receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     induces protein tyrosine phosphorylation. 238:471-478(1999).
                                                                                                                                                                                                                                                                                                                                                                                PF00007; Cys_knot; PF00219; IGFBP; 1.
                      10
                                          9
                                                                                                                                                                                                                                               factor;
                                                                        Similarity
                                  SKTQPCDHTKGLECNFGASSTALKGICRAQSEGRPCEYNSRIYQNGESFQPNCKHQCTCI
                                                                                                                                                                                                                                                                                                                                                                                                                         IPR006208;
IPR006207;
IPR000867;
                      {\tt LCLGFLLLHLLNQVSATLRCPSRCPSQCPSISPTCAPGVRSVLDGCSCCPVCARQRGESC}
                                                                                                                                                                                                                                                                                                                                                                                                               IPR000884;
                                                                                                      351
                                                             Conservative
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                                                                                                      AA;
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                                                                                                               39.4%;
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not; 1.
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that leads t
                                                                     .98;
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                                                             51;
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BY SIMILARITY.

N-LINKED (GLCNAC....
                                                           Score 829.5; I
Pred. No. 3.1e
51; Mismatches
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                                                                                                                                                                                            NOV PROTEIN
IGFBP.
VWFC.
TSP TYPE-1.
                                                                                                                                                                                                                                       POTENTIAL.
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                                                                                                      02619707DE7C1BFB CRC64;
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                                                                       829.5;
No. 3.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    similarity).
                                                             5; DB 1;
8.1e-54;
nes 114;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                codes
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                                                                                  351;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1997
15-SEP-2003
NOV protein
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Q64299;
Q1-NOV-1997
                                                                                                                                                            the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entities requires a license agreement (See http://www.isb-slb.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                       This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genomics [2]
                                                EMBL; X97863; CAA66457.1;
EMBL; Y09257; CAA70454.1;
EMBL; X96585; CAA65404.1;
MGD; MGI:109185; Nov.
                                                                                                                                                                                                                                                                                                                                                                                                \frac{1}{1} \cdot \frac{1}{1} \cdot \frac{1}{1}
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN-129/Sv, and ICR; TISSUE-Brain;
MEDLINE-97131523; PubMed-8975721;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gene protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nephrogenesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Snaith M.R., Natarajan D., Taylor L.B., Cho
Perbal B., Schofield P.N., Boulter C.A.,
"Genomic structure and chromosomal mapping
Genomics 38:425-428(1996).
                          InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=C57BL/6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                     s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                      GROWTH REGULATION (BY SIMILARITY).
SUBUNIT: Interacts with FBLN1 (By similarity).
SUBCLLULAR LOCATION: Secreted.
SIMILARITY: Contains 1 IGFBP domain.
SIMILARITY: Contains 1 VWFC domain.
SIMILARITY: Contains 1 TSP type-1 domain.
SIMILARITY: Contains 1 C-terminal cystine knot-like (CTCK)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              245
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (Rel. 35, Created)
(Rel. 35, Last sequence update)
(Rel. 42, Last annotation update)
homolog precursor (NovH) (Nephroblastoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              homolog).
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Rodentia;
Cys_knot.
Cys_knot_C.
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potential role
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Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Choi C.P.,
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Murinae; Mus
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Best Local
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Pfam; PF000219; IGFBP; 1.
Pfam; PF00090; tsp_1; 1.
Pfam; PF00090; twc; 1.
SMART; SM00041; CT; 1.
SMART; SM00121; IB; 1.
SMART; SM00209; TSP1; 1.
SMART; SM00209; TSP1; 1.
SMART; SM00214; VWC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS01185; CTCK_1
PROSITE; PS01225; CTCK_2
PROSITE; PS00222; IGF_B
PROSITE; PS50092; TSPI;
PROSITE; PS01208; VWFC_1
PROSITE; PS01208; VWFC_1
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InterPro;
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337 NNEA 340
                 360
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                                                                                                                                                                                                                                                   Similarity
                 PNEA
                                                                DCSKTQPCDHTKGLECNFGASSTALKGICRAQSEGRPCEYNSRIYQNGESFQPNCKHQCT
                                                                                                                                                                                                        NCTSLYTYKPRFCGVCSDGRCCTPHNTKTIQVEFQCLPGEIIKKPVMVIGTCTCYSNCPQ
                                          GCSSVKKYRPKYCGSCVDGRCCTPLQTRTVKMRFRCEDGEMFSKNVMMIQSCKCNYNCPH
                                                                                                                                     CIDGAYGCIPLCPQELSLPNLGCPNPRLYKYSGQCCEEWVC--DEDSIKDSLDDQDDLLG
                                                                                                   LPAYRPEATVGVEV----SDSSI-----
                                                                                                                    LDASEVELTRNNELIAIGKGSSLKRLPVFGTEPRVLFNPLHAHGQKCIVQTTSWSQCSKS
                                                                                                                                                                       SCSEMRPCDQSSGLYCDRSADPNNQTGICMV-PEGDNCVFDGVIYRNGEKFEPNCQYFCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IPR000867; Insl_gro_fac_pr.
IPR000884; TSP1.
IPR001007; VWF_C.
                                                                                                                                                                                                                                                                             354
                                                                                                                                                                                                                                           Conservative
                 363
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                                                                                                                                                                                                                                                                                                                                                                                               Signa
                                                                                                                                                                                                                                                                                                                                                                                                                                  CTCK_1; 1.
CTCK_2; 1.
IGF_BINDING;
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VWFC_1
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354
101
168
247
235
298
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312
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277
                                                                                                                                                                                                                                                                            38928 MW;
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CTCK.
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Pred.
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N-LINKED (GLCNAC. . .) (F
08ECE8CFC67829DE CRC64;
                                                                                                                                                                                                                                                                                                                                                                       IGFBP.
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NOV PROTEIN HOMOLOG
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Y SIMILARITY.
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Y SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                       TYPE-1
                                                                                                                                                                                                                                                  827; DB 1;
NO. 4.8e-54;
                                                                                                                                                                                                                                           114;
                                                                                                                                                                                                                                                         Length 354;
                                                                                                   ----NCIEQTTEWSACSKS
                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                   (POTENTIAL).
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                                                                                                                                                                                                                                           Gaps
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                                                                                                                                     182
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                                  336
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NOV_XENLA P51609; 01-OCT-1996 01-OCT-1996 28-FEB-2003

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STANDARD;

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DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS01185; CTCK_1; FALSE_NEG.
PROSITE; PS01225; CTCK_2; 1.
PROSITE; PS00222; IGF_BINDING; 1.
PROSITE; PS50092; TSP1; 1.
PROSITE; PS01208; VWFC_1; 1.
PROSITE; PS01208; VWFC_2; 1.
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SMART; SM00214; VWC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00219; IGFBP; 1.
Pfam; PF00090; tsp_1; 1.
Pfam; PF00093; vwc; 1.
SMART; SM00041; CT; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the chicken nov gene."
Gene 171:243-248(1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. MEDLINE=96257227; PubMed=8666280;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostómi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; U37063; AAB17096.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ying Z., King M.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR006208; Cys_knot.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -1- FUNCTION: IMMEDIATE-EARLY PROTEIN LIKELY TO PLAY A ROLE IN CELL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein homolog precursor (Xnov).
                                                                                                         152;
                                     տ
                                                                                                                                Similarity
IPR001007; VWF_C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IPR006207; Cys_knot_C.
IPR000867; Insl_gro_fac_pr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IPR000884;
                                                                                                                                                                                                  343 AA;
                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                  19
21
93
190
249
249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /; Cys_knot;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Signal
                                                                                                                                                                                                  38070 MW;
                                                                                                                            39.2%; Score 824.5; DB 42.1%; Pred. No. 7e-54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TSP1
                                                                                                         49;
                                                                                                                                                                                                                                     TSP TYPE-1.
CTCK.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                             N-LINKED (GLCNAC. . .) (P
677D7078EB21365F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                    IGFBP.
                                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL.
NOV PROTEIN HOMOLOG.
                                                                                                         Mismatches
                                                                                                                                            DB 1;
                                                                                                         107;
                                                                                                      Indels
                                                                                                                                            Length 343;
                                                                                                                                                                                                                  (POTENTIAL).
                                                                                                         53;
                                                                                                    Gaps
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Db	Qy	рь	Qy	Дb	Qy	Db	Qy	Db	Qy	DЪ	Qy
323	358	263	298	203	239	180	179	123	128	64	68
323 P 323 .	358 P 358	YKNCTSVQPYKPKFCGQCSDGRCCTPHSTKTMHVEFVCPQKRIVKKPVMVISTCVCHYNC 322	YAGCSSVKKYRPKYCGSCVDGRCCTPLQTRTVKMRFRCEDGEMFSKNVMMIQSCKCNYNC 357	KTCGMGVSSRVTNRNARCEMQKQIRLCMVRSCEEEPGWHVEKKGKKCVRVRKTTKPIHFH 262	KSCGTGISTRYTNDNPECRLVKETRICEVRPC-GQPVYSSLKKGKKCSKTKKSPEPVRFT 297	LGIDASDTSFACIAQTTEWSACS 202	LGLDASEVELTRNNELIAIGKGSSLKRLPVFGTEPRVLFNPLHAHGQK	IGCVPRCNLDLLLPGPDCPFPRRVKVPGECCEKWVCDSKEEMAIGGFAMAAYRPEAT 179		NPCQEDKGLYCEFNADPRMETGTCMA-LEGNSCVFDGVVYRNRESFQPSCKYHCTCLNGH 122	QPCDHTKGLECNEGASST!
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Search completed: August 5, 2003, 14:05:36 Job time: 11.475 secs

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Minimum DB
Maximum DB
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence:
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Perfect score:
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ALIGNMENTS

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Q21281 Q964N4 Q9JLLO

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3 Q90XG4 097574 097574 1 035888 095710 094813 094813 Q90Z44 Q8WYK7 Q9UDE4 3 Q9DF21 3 Q9IBG7 Q9T3A6 Q8T3A7

Q9XWD6 Q90Z43

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Ojwyk7 homo sapien
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Ojibg7 xenopus lae
Ojibg8 caenorhabdi
Ojivd6 caenorhabdi
Ojivd6 gallus gall
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Ojivg9 rattus norv
Oj5710 homo sapien
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Signal.	 DROCKTHE DROLLOR VERTO 1	. 5550000.	PS00222:	: PS01225:	PROSITE; PS01185; CTCK_1; 1.	SMART; SM00214; VWC; 1.	SMART; SM00209; TSP1; 1.	SMART; SM00121; IB; 1.	SM00041;	Pfam; PF00093; vwc; 1.		PF00219;	Cys_knot;	InterPro; IPR001007; VWF_C.	IPR000884;	InterPro; IPR000867; Insl_gro_fac_pr.	IPR006207;	InterPro; IPR006208; Cys_knot.	EMBL; AB015877; BAA78339.1;		1 mRNA.";	Unoki H., Yonekura H., Furukawa K., Yamamoto H.;		SEQUENCE FROM N.A.	[1]	NCBI_TaxID=10116;	Eutheria; Rodentia; Sciurognathi; Muridae;	þ	Rattus norvegicus (Rat).	CYR61.	CYR61 precursor.	(TrEMBLrel. 23, Last	01-NOV-1999 (TrEMBLrel. 12, Last sequence update)	1999 (TrEMBLrel.		Q9WTM9 PRELIMINARY; PRT; 379 AA.	K L L

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Best Local S
Matches 372
                                                                                                                                                                                                                                                                    "Characterization of Xenopus cyr61.";
Submitted (NOV-2000) to the EMBL/GenBank/DDBJ date EMBL, AF320592; AAK00947.1;
InterPro; IPR006208; Cys_knot.
InterPro; IPR006207; Cys_knot_C.
InterPro; IPR000867; Insl_gro_fac_pr.
InterPro; IPR000884; TSP1.
InterPro; IPR000884; TSP1.
InterPro; IPR001007; VWF_C.
Pfam; PF00007; Cys_knot_1
                                                                                                                                                                                  InterPro; IPRO0
Pfam; PF00007;
Pfam; PF00219;
Pfam; PF00090;
Pfam; PF00093;
SMART; SM00041;
                                     SMART; SI
PROSITE;
PROSITE;
PROSITE;
PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q98TX5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
101-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Secreted cysteine-rich protein cyrél.
Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIGNAL CHAIN
                                                                                                                                                                       SMART;
Pfam; PF00219; Cys_knot; 1.

Pfam; PF00219; IGFBP; 1.

Pfam; PF00090; tsp_1; 1.

Pfam; PF00093; vwc; 1.

ART; SM00041; CT; 1.

ART; SM000121; IB; 1.

ART; SM000121; IB; 1.

TT; SM00214; VWC; 1.

TT; SM00214; VWC; 1.

TE; PS01185; CTCK_1; 1.

TE; PS01225; CTCK_2; 1.

TE; PS01225; CTCK_2; 1.

TE; PS00222; IGF_BINDING; 1.

E; PS00222; TSP1; 1.
                                                                                                                                               SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
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372; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NEASFRLYSLFNDIHKFRD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CTCIDGAVGCIPLCPQELSLPNLGCPNPRLVKVSGQCCEEWVCDEDSIKDSLDDQDDLLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NEDCSKTQPCDHTKGLECNFGANSTALKGICRAQSEGRPCEYNSRIYQNGESFQPNCKHQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NEDCSKTQPCDHTKGLECNFGASSTALKGICRAQSEGRPCEYNSRIYQNGESFQPNCKHQ
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25
379
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AA;
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98.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 2076;
Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL.
CYR61.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Vertebrata; Euteleostomi;
la; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 11;
1.8e-189;
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                                                                                                                                                                                                                                                                                                                                                                                                                             databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CRC64;
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Q9UID7 .
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SQ
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Best Local
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                                                                                                                     Pfam; PF00007; Cys_knot; Pfam; PF000219; IGFBB; 1. Pfam; PF00090; tsp_1 1. Spfam; PF00093; vwc; 1. SMART; SM00209; TSP; 1. SMART; SM00209; TSP; 1. SMART; SM002041; VWC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAY-2000
01-MAY-2000
01-MAR-2003
                                                                                                                                                                                                                                                                      InterPro;
InterPro;
InterPro;
                                                                                                                                                                                                                                                                                                                                                                              embryonal-rhabdomyosarcoma (RMS).";
Submitted (MAY-1997) to the EMBL/GenBank/DDBJ
EMBL; AF003114; AAF21597.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human)
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS01208; VWFC; 1. SEQUENCE 375 AA; 41460 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CYR61 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9UID7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9UID7
                                                                                                                                                                                                                                                                                                                                         InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                        "Cloning of a new gene down-regulated in the embryonal-rhabdomyosarcoma (RMS).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Anding B., Long Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Kidney;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 1-107 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                          [nterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              359
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; IPR006208; Cys_knot.

; IPR006207; Cys_knot.C.

; IPR000687; Ins1_gro_fac_pr.

o; IPR000884; TSp1.

o; IPR001007; VWF_C.

F00007; Cys_knot; 1.

F00219; IGFBP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                       PS01225; CTCK_2;
PS50092; TSP1; 1.
PS01208; VWFC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EASFRLYSLFNDIHKFRD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GTGISTRVTNDNPECRLVKETRICEVRPCGQPVYSSLKKGKKCSKTKKSPEPVRFTYAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EVELTRNNELIAIGKGSSLKRLPVFGTEPRVLFNPLHAH----GQKCIVQTTSWSQCSKSC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GCIPLCPQELSLPNLGCPNPRLVKVSGQCCEEWVCDEDSIKDSLDDQDDL----LGLDAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EA-YPYYRLFNDIHKFRD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SSVKKYRPKYCGSCVDGRCCTPQQTRTVKIRFRCEDGETFTKNVMMIQSCRCNYNCPHTN
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0 (TrEMBLrel.
3 (TrEMBLrel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                 TSP1; 1.; VWFC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chordata;
Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            77.2%;
77.5%;
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13,
23,
                                     W.
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Last sequence up
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     379
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Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Craniata; Vo
Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                     9188987A7352E948
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            78075CA7B380304E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            No. 1.96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .9e-146;
es 37;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  on update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 small-cell
                                                                                                                                                                                                                                                                                                                                                                                                       databases
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RESULT
Q98TQ8
ID TQ8
ID TQ9
ID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local S
Matches 273
                                                                                                                            Pfam; PF00007; Cys_knot; 1.
Pfam; PF00219; IGFBP; 1.
Pfam; PF00090; tsp_1; 1.
Pfam; PF00090; vwc; 1.
SMART; SW00041; CT; 1.
SMART; SW00121; IB; 1.
SMART; SW00214; VWC; 1.
SMART; SW00214; VWC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q98T08;
Q98T08;
Q1-JUN-2001 (TrEMBLrel. 17, Created)
Q1-JUN-2001 (TrEMBLrel. 17, Last sequence update)
Q1-JUN-2001 (TrEMBLrel. 23, Last annotation update)
Q1-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Connective tissue growth factor precursor (Connective factor/hypertrophic chondrocyte-specific protein 24).
Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eu
                  PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
                                                                                                                                                                                                                                                                                                  InterPro; IPR006208; Cys_knot.
InterPro; IPR006207; Cys_knot_C.
InterPro; IPR006867; Insl_gro_fac_pr.
InterPro; IPR000884; TSP1.
InterPro; IPR001007; VWE_C.
                                                                                                                                                                                                                                                                                                                                                                                                                     Mukudai Y., Kubota S., Takic Submitted (DEC-2001) to the EMBL; AJ298335; CAC33438.1; EMBL; AF463517; AAL68834.1;
Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Archosauria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N
                  PS01185; CTCK_1; 1.
PS01225; CTCK_2; 1.
PS00225; IGE_BINDING; PS00222; TSP1; 1.
PS0092; TSP1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NGESFQPNCKHQCTCIDGAVGCIPLCPQELSLPNLGCPNPRLVKVSGQ:CEEWVCDEDSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GEMFSKN----VMMIQSCKCNYNCPHPNEASFRLYSLFNDIHKFRD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GCGCCKVCAKQLNEDCSKTQPCDHTKGLECNFGASSTALKGICRAQSE(;RPCEYNSRIYQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GDIFQERHDDPVL----KCNYNCPHANEAAFPFYRLFNDIHKFRD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NGESFQPNCKHQCTCIDGAVGCIPLCPQELSLPNLGCPNPRLVKVTGQ::CEEWVCDEDSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GCGTHPNLCIHLGHTASPTSYKHHTKGLECNFGASSTALKGICRAQSE(;RPCEYNSRIYQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (JAN-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     etazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           69.2%;
78.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Takigawa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 1455; DI
Pred. No. 2.3e
13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3
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.3e-130;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ΑA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 databases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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Best Local S
Matches 170
Pfam; PF00007; Cys_knot; 1
Pfam; PF00007; tsp_1; 1.
Pfam; PF00099; tsp_1; 1.
Pfam; PF00099; vwc; 1.
SMART; SM00041; CT; 1.
SMART; SM00121; IB; 1.
SMART; SM00209; TSP1; 1.
SMART; SM00204; VWC; 1.
PROSITE; PS01185; CTCK_1;
PROSITE; PS01125; CTCK_1;
PROSITE; PS01208; VWFC; 1.
                                                                                                                                                                             SEQUENCE FROM N.A.
Ying Z., King M.L.;
Submitted (AUG-1997) to the
EMBL; U43524; AAB67639.1;
EMBL; U43523; AAB67638.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIGNAL
CHAIN
SEQUENCE
                                                                                                                        InterPro; IPR006208; Cys_knot.
InterPro; IPR0086207; Cys_knot_C.
InterPro; IPR000867; Insl_gro_fac_pr.
InterPro; IPR000884; TSP1.
InterPro; IPR001007; VWF_C.
                                                                                                                                                                                                                                                                                     01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation updat
Connective tissue growth factor XCTGF.
Xenopus laevis (African clawed frog).
                                                                                                                                                                                                                                                                                                                                           042607;
                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata;
Amphibia; Batrachia; Anura; Me
                                                                                                                                                                                                                                              NCBI_TaxID-8355;
                                                                                                                                                                                                                                                         Xenopodinae;
                                                                                                                                                                                                                                                                                                                                                                          G
                                                                                                                                                                                                                                                                                                                                                                                                          332
                                                                                                                                                                                                                                                                                                                                                                                                                              365
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          al Similarity
170; Conser
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ESLYYRKMYGDM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KTQPCDHTKGLECNFGASSTALKGICRAQSEGRPCEYNSRIYQNGESFQPNCKHQCTCID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FRLY--SLFNDI 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                   KKYRPKYCGSCVDGRCCTPLQTRTVKMRFRCEDGEMFSKNVMMIQSCKCNYNCPHPNEAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VELTRNNELIAIGKGSSLKRL-PVFGTEPRVLFNPLHAHGQKCIVQTTSWSQCSKSCGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ERDPCDHKGLFCDFGSPANRRIGVCTAR-DGAPCVFSGMVYRSGESFQSSCKYQCTCLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SLAVALLLALLGPEVRGQECSGQCQCGSGPGPSCPAGVSLVLDGCGCCRVCAKQLGELCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----AKEQTAVGPALAAYRLEDTYGPDPTMM-----RANCLVQTTEWSACSKTCGMG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GAVGCVPLCSMDVRLPSPDCPYPRRVKLPGKCCEEWVCDE:
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22
344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       44.6%;
llarity 45.7%;
Conservative 61
                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                        Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AA;
  CTCK_2;
TSP1; 1
VWFC; 1
                     CTCK_1; 1.
CTCK_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21
344
37499
                                                                                                                                                                                                                                                                                                                                                                                                         343
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Score 938; DB 13;
; Pred. No. 4.4e-81;
61; Mismatches 103;
                                                                                                                                                                                                                                                                  a; Craniata; Ven
Mesobatrachia;
                                                                                                                                                                                                     EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL.
CONNECTIVE TISSUE GROWTH FACTOR
5 69E639AF69BF1D00 CRC64;
                                                                                                                                                                                                                                                                                                                                                     343
                                                                                                                                                                                                                                                                             Vertebrata;
                                                                                                                                                                                                                                                                                                                                                     A
                                                                                                                                                                                                                                                                  rtebrata; Euteleostomi;
Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                          update)
                                                                                                                                                                                                      databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            125
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EQ

170 188 128

70 89

129

361 271 301 211 241

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Q
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Best Local :
                                                                                                                                               MEDLINE-99033008; PubMed-9813273;
Cash D.E., Gates P.B., Imokawa Y., Brockes J.P.;
"Identification of newt connective tissue growth fa
retinoid regulation in limb blastenal cells.";
Gene 222:119-124(1998).
EMBL; AJ271167; CAB65965.1; -
InterPro; IPR006208; Cys_knot.
InterPro; IPR006207; Cys_knot_C.
InterPro; IPR000867; Insl_gro_fac_pr.
InterPro; IPR000884; Tsp1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAY-2000
01-MAY-2000
01-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9PT80;
               SMART;
SMART;
                                                                                                     Pfam;
Pfam;
                                                                           Pfam;
                                                                                         Pfam;
                                                                                                                                                                                                                                                                                                                                                                        TISSUE-Forelimb
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Notophthalmus viridescens (Eastern newt) (Triturus viridescens).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Caudata; Salamandroidea; Salamandridae;
                                            SMART;
                                                            SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                      InterPro;
                                                                                                                                                                                                                                                                                                    TISSUE=Forelimb
                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Notophthalmus
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                                                                           PF00093;
                                           SM00041;
SM00121;
                                                                                                                      PF00007;
               SM00209;
SM00214;
                                                                                          PF00090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CPAACHCPLEAPKCAPGYGLVRDGCGCCKVCAKQLNEDCSKTQPCDHTKGLECNFGASST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HRTATLPVEFKCPDGEVMKKNMMFIKTCACHFNCPGDNDIFEAMYYRKMYGDM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LQTRTVKMRFRCEDGEMFSKNVMMIQSCKCNYNCPHPNEASFRLY--SLFNDI: | : |: | : |: : |: : |:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PNPRLVKVSGQCCEEWVCDEDSIKDSLDDQDDLLG--LDASEVELTRNNELIAIGKGSSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RKIGVCTAR-EGAPCVFGGTVYRSGESFQSSCKYQCTCIDGGVGCVPLCSMDIRLPSPEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ALKGICRAQSEGRPCEYNSRIYQNGESFQPNCKHQCTCIDGAVGCIPLCPQELSLPNLGC
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                                                                                                                                      IPR001007;
                                                                                                                                                                                                                                                                                                                                              (JAN-2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (TrEMBLrel. 13, Created)
(TrEMBLrel. 13, Last sequence up
(TrEMBLrel. 23, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
             Cys_knot;
; IGFBP; 1.
; tsp_1; 1.
; vwc; 1.
; CT; 1.
1; IB; 1.
1; IB; 1.
9; TSP1; 1.
                                                                                                                                                                                                                                                                                                                                                                          l.A.
blastema;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ä,
                                                                                                                                                                                                                                                                                                    blastema;
CTCK_1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          growth
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                                                                                                                                   VWF_C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                44.68;
                                                                                                                                                                                                                                                                                                                                              to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 937; DB
Pred. No. 5.5e
60; Mismatches
                                                                                                                                                                                                                                                                                                                                              EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           93F221C5DB565A81 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  347
                                                                                                                                                                                                                                        ssue growth cells.";
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.5e-81;
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                                                                                                                                                                                                                                                                                                                                              databases
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                                                                                                                                                                                                                                                         target
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      374
                                                                                                                                                                                                                                                         of.
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097765
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Best Local
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01-MAY-1999
01-MAR-2003
Pfam; I
SMART;
SMART;
SMART;
SMART;
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PROSITE;
PROSITE;
PROSITE;
SEQUENCE
                                                                                       Pfam;
                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              097765
                                                                         Ptam;
                                                                                                       Pfam;
                                                                                                                     InterPro;
                                                                                                                                   InterPro;
                                                                                                                                                InterPro;
                                                                                                                                                                                               EMBL; U70060; AAD00174.1;
                                                                                                                                                                                                           Submitted (SEP-1996) to the
                                                                                                                                                                                                                                                      Harding P.A.,
                                                                                                                                                                                                                                                                      TISSUE=Uterus;
                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                            Sus scrofa
                                                                                                                                                                                                                                                                                                                                                                                         Connective tissue
                                                                                                                                                                 InterPro;
                                                                                                                                                                              InterPro;
                                                                                                                                                                                                                            (CTGF) cDNA.";
                                                                                                                                                                                                                                       "Cloning and
PF00093; v
1; SM00041;
1; SM00121;
5; SM00209;
2; SM00214;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       332
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                                                                                       PF00007;
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                                                                         PF00090;
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;; PS00222; IGF_BINDING; 1
;; PS00222; TSP1; 1.
;; PS01208; VWFC; 1.
;; PS01208; VWFC; 1.
                                                                                                  p; IPR006208; Cys_knot.
o; IPR006207; Cys_knot_C.
o; IPR000867; Insl_gro_fac_pr.
o; IPR000884; Tsp1.
o; IPR001007; VWF_C.
F00007; Cys_knot; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DIFESMYYRKMYGDM
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                                                                                                                                                                                                                                                                                                                                                          (Pig).
                                                                                                                                                                                                                                                                                                                                                                                      (TIEMBLIE1. 10, Created)
(TIEMBLIE1. 10, Last sequence update)
(TIEMBLIE1. 23, Last annotation update)
tissue growth factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                       sequencing
            Cys_knot;
IGFBP; 1.
tsp_1; 1.
twc; 1.
vwc; 1.
; CT; 1.
l; CT; 1.
l; IB; 1.
                                                                                                                                                                                                                                                      Brigstock
                                                                                                                                                                                                                                                                                                                             Chordata; Craniata; Ver
Cetartiodactyla; Suina;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      43.8%;
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of a p
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   374
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        54;
                                                                                                                                                                                                            EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 920.5; DB 13;
Pred. No. 2.1e-79;
4; Mismatches 103;
                                                                                                                                                                                                                                        porcine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
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                                                                                                                                                                                                                                          connective
                                                                                                                                                                                                                                                                                                                                                                                                                                                                349
                                                                                                                                                                                                                                                                                                                               Vertebrata;
ina; Suidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Å
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Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      347;
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                                                                                                                                                                                                                                          factor
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Best Local :
                                                                                                      Matches
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PROSITE;
PROSITE;
PROSITE;
PROSITE;
                                                                                                                                                                                 the RIKEN Genome Exploration Research Group "Analysis of the mouse transcriptome based c60,770 full-length cDNAs.";
Nature 420:563-573(2002).
EMBL, AK039481; BAC30363.1; -
                                                                                                                                                                                                                                                          The
the
                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN-C57BL/6J; TISSUE-Spinal cord;
MEDLINE-22354683; PubMed-12466851;
                                                                                                                                                                                                                                                                                                                                                                                                                                             08CA67;
01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last seq
01-MAR-2003 (TrEMBLrel. 23, Last ann
                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
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; PS01225; CTCK_2; 1.
; PS00222; IGF_BINDING; ; PS50022; TSP1; 1.
; PS01208; VWFC; 1.
; PS01208; VWFC; 1.
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DCSKTQPCDHTKGLECNFGASSTALKGICRAQSEGRPCEYNSRIYQNGESFQPNCKHQCT 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FQPNCKHQCTCIDGAVGCIPLCPQELSLPNLGCPNPRLVKVSGQCCEE;WCDEDSIKDSL 172
                                                                 RTLAVAVTLLH-LTRLALS-TCPAAC--HCPLEAPKCAPGVGLVRDGCGCCKVCAKQLNE
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                                                                                                                 Score 827; DB 11;
Pred. No. 1.7e-70;
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                                                                       GCSSVKKYRPKYCGSCVDGRCCTPLQTRTVKMRFRCEDGEMFSKNVMMIQSCKCNYNCPH
                                                                                                                                CGTGISTRYTNDNPECRLYKETRICEVRPCGQ-PVYSSLKKGKKCSKTKKSPEPVRFTYA 299
                                                                                                                                                                                           LDASEVELTRNNELIAIGKGSSLKRLPVFGTEPRVLFNPLHAHGQKCIVQTTSWSQCSKS
                                                                                                                                                                                                                                                                                          NCTSLYTYKPRFCGVCSDGRCCTPHNTKTIQVEFQCLPGEIIKKPVMVIGTCTCYSNCPQ
                                                                                                                  CGMGVSTRVTNRNRQCEMVKQTRLCIVRPCEQEPEEVTDKKGKKCLRTKKSLKAIHLQFE
                                                                                                                                                                           LPAYRPEATVGVEV----SDSSI-----
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01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Connective tissue growth factor related protein WISP-1. Homo sapiens (Human). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 095388 095388 SEQUENCE FROM N.A. NCBI_TaxID=9606; 9 PRELIMINARY; PRT; 367 ₽ Euteleostomi;

TISSUE=Lung, and Fetal kidney; MEDLINE=99061933; PubMed=9843955; Roy M.A., Lawrence I ew M., Watanabe C., C Goddard A.D., Hillan

MEDLINE-990bly3; runner, Welsh J.W., Roy M.A., La Pennica D., Swanson T.A., Welsh J.W., Roy M.A., La Brush J., Taneyhill L.A., Deuel B., Lew M., Watan Melham M.F., Finley G.G., Quirke P., Goddard A.D. Gurney A.L., Botstein D., Levine A.J., Gurney A.L., Botstein D., Levine A.J., "Wilsp genes are members of the connective tissue" "Wilsp genes are members of the c that are up-regulated in wnt-1-transformed cells are expressed in human colon tumors."; Proc. Natl. Acad. Sci. U.S.A. 95:14717-14722(1998). Blechschmidt K., Jonge R.d., Schi EMBL; Rosenthal InterPro; Genew; EMBL; SEQUENCE FROM N.A. AF100779; AAC96321.1; -. AF192304; AAF22341.1; -. HGNC:12769; WISP1. IPR006208; Cys_knot.
IPR006207; Cys_knot_C.
IPR000867; Insl_gro_fac_pr.
IPR000884; TSP1. (OCT-1999) Schilhabel Kalaydjieva L., Goodn Lhabel M., Schattevoy ţo the EMBL/GenBank/DDBJ Goodman F R., Greshar Dette M., Gresham D., growth factor and aberrantly Menzel D.A., Cohen R.L., Lee family

arbro; IPR001007; VWE_C.
n; PF00007; Cys_knot; 1.
n; PF00007; Cys_knot; 1.
n; PF00090; tsp_1; 1.
n; PF00090; twc; 1.
n; PF00093; vwc; 1.
n; PF00093; vwc; 1.
n; SM00011; IB; 1.
rr; SM000214; VWC; 1.
rr; SM000214; VWC; 1.

PS01185; CTCK_1; PS01225; CTCK_2;

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Best Loc
Matches
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MEDLINE=98119879; PubMed=9449709;
Hashimoto Y., Shindo-okada N., Tani M., Nagamar Shiroishi T., Toma H., Yokota J.;
"Expression of the Elm1 gene, a novel gene of "Expression of the Elm1 gene, a novel gene of tissue growth factor, Cyr61/Cef10, and neurobl tissue growth factor, I vivo tumor growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUN-1998
01-JUN-1998
01-MAR-2003
Pennica D., Swanson T.A., Welsh J.W., Roy M.A., Lawrence D Brush J., Taneyhill L.A., Deuel B., Lew M., Watanabe C., C Melham M.F., Finley G.G., Quirke P., Goddard A.D., Hillan Gurney A.L., Botstein D., Levine A.J.;
"MISP genes are members of the connective tissue growth fa that are up-regulated in wnt-1-transformed cells and aberr expressed in human colon tumors.";
Proc. Natl. Acad. Sci. U.S.A. 95:14717-14722(1998).
                                                                                                                                                                                 TISSUE=Mammary gland;
MEDLINE=99061933; PubMed=9843955;
                                                                                                                                                                                                                                                                        gene) family, suppresses in vivo murine melanoma cells.";
J. Exp. Med. 187:289-296(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse
Eukaryota; Metazoa;
Mammalia; Eutheria;
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SEQUENCE
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; PS01208; VWFC;
367 AA; 4033;
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Metazoa; Chordata; Chord
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Last sequence update)
Last annotation updat
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Pred. No. 2.5e-65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Craniata; Vertebrata;
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           361
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                                                                                                                                                                                                                                                                                                                   neuroblastoma overexpressed growth and metastasis of K-1735
                                                                                                                                                                                                                                                                                                                                                                                                             Nagamachi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Muridae;
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; Murinae; Mus
                                               aberrantly
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Cohen
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                                                                                                                                      R.L.,
                                                                                                                                                         Lee
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PROSITE; PS01225; CTCK_2; I
PROSITE; PS01225; TSP1; 1.
PROSITE; PS01208; VWFC; 1.
SEQUENCE 367 AA; 40702 N
                                                                                                                        Q99PPO;
Q99PPO;
01-JUN-2001
01-JUN-2001
01-MAR-2003
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Pfam; PF00093; vs
SMART; SM00041; cs
SMART; SM00121; s
SMART; SM00209; s
SMART; SM00214; v
                                                                                                     ELM1
SEQUENCE FROM N.A.
MEDLINE=20487548; PubMed=11031104;
Sleeman M.A., Murison J.G., Strach
McGrath A., Bickerstaff P., Griers
                                                                   Eukaryota; Metazoa;
Mammalia; Eutheria;
                                               NCBI_TaxID=10116;
[1]
                                                                                         Rattus norvegicus
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InterPro; IPR006207;
InterPro; IPR000867;
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EMBL; AF100777; AAC96319
MGD; MGI:1197008; Wisp1.
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hes 143;
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                                                                                                                                                                                                                                                  PNEASFRLYSLFNDIHKFRD
                                                                                                                                                                                                                                                                         GCVSTRTYRPKYCGVCTDNRCCIPYKSKTISVDFQCPEGPGFSRQVLWINACFCNLSCRN
                                                                                                                                                                                                                                                                                              GCSSVKKYRPKYCGSCVDGRCCTPLQTRTVKMRFRCEDGEMFSKNVMMIQSCKCNYNCPH
                                                                                                                                                                                                                                                                                                                     TCGLGISTRISNVNARCWPEQESRLCNLRPCDVDIQLHIKAGKKCLAVYQPEEATNFTLA
                                                                                                                                                                                                                                                                                                                                          SCGTGISTRVTNDNPECRLVKETRICEVRPCGQPVYSSLKKGKKCSKTKKSPEPVRFTYA
                                                                                                                                                                                                                                                                                                                                                                                      GLDASEVELTRNNELIAIGKGSSLKRLPVFGTEPRVLFNPLHAHGQKCIVQTTSWSQCSK
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IPR001007;
                                                                                                                        (TrEMBLrel. (TrEMBLrel. (TrEMBLrel.
                                                                                                                                                                      PRELIMINARY;
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AAC96319.1;
                                                                   s (Rat).
Da; Chordata;
ia; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            40702 MW;
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; VWF_C.
knot; 1.
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Cys_knot_C.
Insl_gro_fac_pr.
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23,
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Last sequence up
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5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 758.5;
                                                                  Craniata; Ver
Sciurognathi;
                                                                                                                                                                       PRT;
                                                                                                                                                                                                                               361
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                                                                                                                                                                       367
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.6e-64;
.~ 135;
                                                                               Vertebrata;
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                                                                                                                                     update)
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                                                                    Muridae;
                                                                                                                          update)
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                                                                               Euteleostomi;
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                                                                   Rattus
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Strachan Grierson

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Kumble K.D., Havukkala I.,

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Pfam; PF00093; vwc; 1.
SMART; SM00041; CT; 1.
SMART; SM00121; IB; 1.
SMART; SM00209; TSP1; 1.
SMART; SM00214; VWC; 1.
                                                                                                                                                                                                                                                095958;
01-MAY-1999 (TrEMBLrel. 10, C
01-MAY-1999 (TrEMBLrel. 10, I
01-MAR-2003 (TrEMBLrel. 23, I
DJ142L7.3 (Connective tissue
                                                                                                                  Homo sapiens (Human
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE;
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DJ142L7.3 OR LIBC.
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                                SEQUENCE FROM N.A
                                                                                       NCBI_TaxID=9606;
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n; PF00219; IGFBP;
n; PF00090; tsp_1;
n; PF00093; vwc; 1.
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145; Conserv
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PS01225;
PS50092;
PS01208;
367 AA;
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IPR000867; Insl_gro_fac_pr.
IPR000884; TSP1.
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etazoa; Chordata;
theria; Primates;
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Last annotation update)
e growth factor (NOV, GI
                                                                                                                                                                                                                                                                                                                                           Created)
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Pred. No. 8
                                                                                                            Craniata; Vertebrata; Catarrhini; Hominidae
                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
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                                                                                                                  Hominidae;
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Pfam; PF0002019; IGFBP; 1.
Pfam; PF000090; tsp_1; 1.
SMART; SM00041; CT; 1.
SMART; SM00121; IB; 1.
SMART; SM00125; TSP1; 1.
PROSITE; PS01225; CTCK_2; 1.
                                                                                                                                                                                                                                                   01-MAY-1999 (TIEMBLIEL 10, Created)
01-MAY-1999 (TIEMBLIEL 10, Last sequence update)
01-MAY-3999 (TIEMBLIEL 23, Last annotation update)
01-MAR-2003 (TIEMBLIEL 23, Last annotation update)
Connective tissue growth factor related protein W
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted [2]
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TISSUE=Bone
                                                                                                                           Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                            WISP3
                                                                                                                                                                                                                                                                                                                                                                                        095389;
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                                 SEQUENCE FROM
                                                                                             NCBI_TaxID=9606;
                                                                                                                                                                                          Homo sapiens
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EMBL; AF143679; AAD31517.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SYKTMPAYRNLPLI --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SLKRLPVFGTEPRVLFNPLHAHGQKCIVQTTSWSQCSKSCGTGISTRVTNDNPECRLVKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---CPNPRLVKVSGQCCEEWVCDEDSIKDSLDDQDDLLGLDASEVELTRNNELIAIGKGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PS00222;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CCTPLQTRTVKMRFRCEDGEMFSKNVMMIQSCKCNYNCPHPNE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TRICEVRPCGQPVYSSLK--KGKKCSKTKKSPEPVRFTYAGCSSVKKYRPKYCGSCVDGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GSHCSGAK - - - - GGKKSDQSNCSLEPLLQQL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RYETGYCACKSYG--CEFNQVHYHNGQYFQPNPLFSCLCYSGAIGCTP----LFIPKLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CHWPCKCPQQKPRCPPGVSLVRDGCGCCKICAKQPGEICNEADLCDPHKGLYCDYSVDRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IPR006208; Cys_knot.
IPR006207; Cys_knot_C.
IPR000867; Insl_gro_fac_pr.
IPR000884; TSP1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      331 AA;
marrow,
                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                       (Human).
                                 N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTCK_2; 1. IGF_BINDING;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TSP1;
                                                                                                                           Chordata;
Primates;
and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30.28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      36909
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Fetal kidney;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 635.5; |
Pred. No. 2.8e
57; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   --WKKKCLVQATKWTPCSRTCGMGISNRVTNENSNCEMRKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL/GenBank/DDBJ
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                                                                                                                           Craniata; V
Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      D109C2FDCA1DF549 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                   354
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                                                                                                                                                                                                                                                tion update)
protein WISP-3.
                                                                                                                                                            Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                   A
                                                                                                                              Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     databases
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                                                                                                                                                            Euteleostomi;
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RESULT
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DT QE
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Pfam; PF00090; tsp_1; 1.

SMART; SM00041; CT; 1.

SMART; SM00101; IB; 1.

SMART; SM001029; TSP1; 1.

SMART; SM00209; TSP1; 1.

PROSITE; PS001225; CTCK_2; 1.

PROSITE; PS001225; IGF_BINDING; 1.

PROSITE; PS0092; TSP1; 1.

SEQUENCE 354 AA; 39292 MW: 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local
  EMBL;
                                                                                                                                                                                                                                           QBCIC8 PRELIMINARY; PRT; 251 AA.

QBCIC8;
01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Similar to WNT1 inducible signaling pathway protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       that are up-regulated in wnt-1-transformed cells are expressed in human colon tumors.";

Proc. Natl. Acad. Sci. U.S.A. 95:14717-14722(1998).

EMBL; AF100781; AAC96323.1; -.

Genew; HGNC:12771; WISP3.
                            Submitted
                                                 Strausberg R.;
                                                              SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE-Mammary gland;
                                                                                                                                                                                                  Mus musculus (Mouse)
Eukaryota; Metazoa; (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pennica D., Swanson T.A., Welsh J.W., Roy M.A., Lawrence D.A., Brush J., Taneyhill L.A., Deuel B., Lew M., Watanabe C., Cohen Melham M.F., Finley G.G., Quirke P., Goddard A.D., Hillan K.J., Gurney A.L., Botstein D., Levine A.J.;
                                                                                                                                                   NCBI_TaxID=10090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          320
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tted (JUN-2002)
BC032877; AAH3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       genes are members of the connective tissue growth factor family are up-regulated in wnt-1-transformed cells and aberrantly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         86
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TRICEVRPCGQPVYSSLK--KGKKCSKTKKSPEPVRFTYAGCSSVKKYRPKYCGSCVDGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CCIPNKSKMITIQFDCPNEGSFKWKMLWITSCVCQRNCREPGD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SYKTMPAYRNLPLI-----WKKKCLVQATKWTPCSRTCGMGISNRVTNENSNCEMRKE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GSHCSGAK----GGKKSDQSNCSLEPLLQQL------
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IPR006207; Cys_knot_C.
IPR000867; Insl_gro_fac_pr.
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  AAH32877.1;
                                                                                                                                                                             Rodentia;
                                                                                                                                                                                               Chordata;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 622; DB Pred. No. 5.9e 56; Mismatches
                         EMBL/GenBank/DDBJ
                                                                                                                                                                                                    Craniata;
                                                                                                                                                                          Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          67F48D0D5C2F5EE3 CRC64;
                                                                                                                                                                                                    Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 4;
.9e-51;
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                                                                                                                                                                          Muridae;
                            databases
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                                                                                                                                                                                                    Euteleostomi;
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                                                                                                                                                                          Murinae;
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00007; Cys_knot;
Pfam; PF000219; IGFBP; 1.
Pfam; PF000090; tsp_1; 1.
SMART; SM00041; CT; 1.
SMART; SM00121; IB; 1.
SMART; SM00209; TSP1; 1.
                                                                                                                                                                                                                                                                                                                            PROSITE; PS01185; CTCK_1;
PROSITE; PS01225; CTCK_2;
PROSITE; PS50092; TSP1; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tanaka S., Sugimachi K.;
"Human WISP-1 variant.";
"Human (NOV-1999) to the EMBL/GenBank/DDBJ EMBL; AB034725; BAB17849.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAR-2001 (TrEMBLrel. 01-MAR-2003 (TrEMBLrel. WISP-1 variant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR006208; Cys_knot.
InterPro; IPR006207; Cys_knot_C.
InterPro; IPR000867; Insl_gro_fac_pr.
InterPro; IPR000884; TSP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9HCS3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9HCS3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15
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  122
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                                             85
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IDGAVGCIPLCPQELSLPNLGCPNPRLVKVSGQCCEEWVCDEDSIKDSLDDQDDLLGLDA
  TCIDGAVGCIPLCPQELSLPNLGCPNPRLVKVSGQCCEEWVCDEDSIKDSLDDQDDLLGL
                                             DNCTEAAICDPHRGLYCDY
                                                                                   EDCSKTQPCDHTKGLECNFGASSTALKGICRAQSEGRPCEYNSRIYQNGESFQPNCKHQC
                                                                                                                              LSPAPTTMDFTPAPLEDTSSRPQFCKWPCECPPSPPRCPLGVSLITDGCECCKMCAQQLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GIATRVSNQNRFCQLEIQRRLCLSRPC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEVELTRNNELIAIGKGSSLKRLPVFGTEPRVLFNPLHAHGQKCIVQTTSWSQCSKSCGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CDHLHVCNPSQGLVCQPGAGPSGRGVVCLFEEDDGSCEVNGRRYLDGETFKPNCRVLCRC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CSKTQPCDHTKGLECNFGASSTALKGICRAQSEGRPCEYNSRIYQNGESFQPNCKHQCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LIHL--LAISFLCILSMVYAQLCPAPCACPWTPPQCPPGVPLVLDGCGCCRVCARRLGES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LLHLTRLALS-----TCPAACHCPLEAPKCAPGVGLVRDGCGCCKVCAKQLNED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DDGGFTCLPLCSEDVRLPSWDCPRPRRIQVPGRCCPEWVCDQAVMQPAI
                                                                                                                                                                                                                                                                                                        280 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  251
                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----QPSSAQ-----GHQLSALVTPASADG-PCPNWSTAWGPCSTTCGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           knot;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chordata;
Primates;
                                                                                                                                                                                                                                         23.8%; 28.6%;
                                                                                                                                                                                                                                                                                                          30697 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27106 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16,
16,
23,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. 2.96
l; Mismatches
                                                                                                                                                                                                                                         Score 499.5;
Pred. No. 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 518.5;
Pred. No. 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Craniata; Vertebrata; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                        26B254D4A060738E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  57520309A9069524 CRC64;
                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             280
                                                                                                                                                                                                                                         .1e-39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .9e-41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A
                                             -SGDRP-----RYAIGV-----CAH--
                                                                                                                                                                                                                                                             DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         update)
                                                                                                                                                                                                                      ; 68
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           databases
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                                                                                                                                                                                                                                                             280;
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Search Job tin	Db	Qy	DЪ	Qy	DЪ	Оу	Db	Qy	Db
Search completed: August 5, 2003, 14:06:50 Job time : 35.9132 secs	264 DIFADLESYPD 274	362 EASFRLYSLFNDIHKFRD 379	204 ISTRSYQPKYCGVCMDNRCCIPYKSKTIDVSFQCPDGLGFSRQVLWINACFCNLSCRNPN 263	302 SSVKKYRPKYCGSCVDGRCCTPLQTRTVKMRFRCEDGEMFSKNVMMIQSCKCNYNCPHPN 361	144 GLGVSTRISNVNAQCWPEQESRLCNLRPCDVDIHTLIKAGKKCLAVYQPEASMNFTLAGC 203	242 GTGISTRVINDNPECRLVKETRICEVRPCGQPVYSSLKKGKKCSKTKKSPEPVRFTYAGC 301	121EVEAWHRN	182 DASEVELTRNNELIAIGKGSSLKRLPVFGTEPRVLFNPLHAHGQKCIVQTTSWSQCSKSC 241	118AVG 120

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Maximum DB
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Gapop 10.0 , Gapext 0.5
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SIDSI/gcgdata/geneseq/geneseqp-embl/AA198, DAT:

SIDSI/gcgdata/geneseq/geneseqp-embl/AA198, DAT:

SIDSI/gcgdata/geneseq/geneseqp-embl/AA199, DAT:

SIDSI/gcgdata/geneseq/geneseqp-embl/AA2000, DAT:
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4	AAR31599	AAY44754	ABB09204	ABP68624	AAB48831	AAB60664	AAB90791	AAB84598	AAE05923	AAY44755	AAY92940	AAY92939	AAW81425	AAY18361	AAW62084	AAW11302	AAW09089	AAR79964	AAY93340	AAW12694	ABB09205	AAE05922	AAY44756	AAW35731	AAR25566	AAY24379	ABB09203	AAE05939	ABB09201	AAE05920	AAR25565	AAE18108	AAY31620	AAR90919	0
ov pr	=	Bovine connective	Human ctgf CNN fam	Human pancreatic c	Human connective t	Human connective t	Human shear stress	Amino acid sequenc	Human connective t	Human connective t	Human connective t	Human connective t	Connective tissue	Human connective t	Human connective t	Connective tissue	Human connective t	Connective tissue	Amino acid sequenc	Connective tissue	Fisp-12 CNN family	Mouse fibroblast s	Mouse connective t	Murine Fisp12. Mu	Beta-IG-M2. Mus m	eti	ce10 C	10 pro	Mouse cyr6 CNN fam	Mouse cysteine-ric	Beta-IG-M1. Mus m	Human alternative	TGF-2.	S	HCGF CNN family pr

ALIGNMENTS

AAW35730;

AAW35730 standard;

Protein;

381 ΑA

27-MAR-1998

(first entry)

ARESULT 1

AAW35730

ID AAW3

XX AAW3

AC AAW3 Cysteine rich protein 61; Cyr61; human; extracellular matrix signalling molecule; cell adhesion; cell migration; cell proliferation; anglogenesis; chondrogenesis; oncogenesis; haematostasis; wound healing; organ regeneration. WPI; 1997-470875/43. N-PSDB; AAT94699. 15-MAR-1996; 14-MAR-1997; 18-SEP-1997 WO9733995-A2 Homo sapiens Human cysteine rich protein 61 (Cyr61). (MUNI-) MUNIN CORP. 96US-0013958 97WO-US04193

protein,

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RESULT 2
AAE05921
ID AAE0
XX AAE0
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                                                    Cysteine-rich protein; Cyr61; extracellular matrix signalling molecule; fibroblast secreted protein; Fisp12; connective tissue growth factor; CTGF; ECM; cell adhesion; cell migration; fibroblast cell proliferation; angiogenesis; wound healing; integrin receptor; atherosclerosis; tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         haematostasis, induce wound healing in a tissue, promote organ regeneration, improve tissue grafting or promote bone or prothesis implantation (claimed). It can also be used to screen for a modulator of angiogenesis, chondrogenesis, oncogenesis, cell adhesion, cell migration, cell proliferation, expand a population of undifferentiated haematopoietic stem cells in culture and to screen for a mitogen (claimed). Ex vivo methods for using mammalian extracellular matrix signalling molecules to prepare blood products are also provided.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Isolated modulate
                                        angiogenesis;
heart disease;
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15-MAY-2000;
06-OCT-2000;
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              KELGFDASEVELTRUNELIAVGKGRSLKRLPVFGMEPRILYNPLQGQKCIVQTTSWSQCS
                                                                            CTCIDGAVGCIPLCPQELSLPNLGCPNPRLVKYTGQCCEEWVCDEDSIKDPMEDQDGLLG
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KELGFDASEVELTRNNELIAVGKGRSLKRLPVFGMEPRILYNPLQGQKCIVQTTSWSQCS
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; 2000US-0204364.
; 2000US-0238705.
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212..281
/note= "Domain III"
282..381
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Best Local S
Matches 379
                                                                                                                                                                                                                                                                                                                                                                                       The present sequence represents a monocyte mature differentiation factor (MMDF) which maintains the life of macrophages for long per in liquid culture. MMDF can be used as an anti-cancer agent, an ir activator and to treat infectious diseases.
                                                                                                                                                                                                                                                                                                                                                        Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A monocyte mature differentiation factor - tissue culture of macrophage(s)
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                                                                     CTCIDGAVGCIPLCPQELSLPNLGCPNPRLVKVTGQCCEEWVCDEDSIKDPMEDQDGLLG
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Pred. No. 1.2e-161;
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DNA sequences, proteins useful in diagnosis and arteriosclerosis -
                                                                                                                                                                                                           The present invention provides the protein and coding sequences of number of human shear stress response proteins. These are useful in diagnosis, treatment and screening of vascular diseases caused by arteriosclerosis, including heart failure, post-PTCA restenosis and
                                                                                                                                                                                                                                                                               Claim 60; Page 345-346; 678pp; Japanese
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Kuga T, Sekine S,
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The present invention relates to a method of inhibiting proliferation of uterine leiomyoma or preventing uterine leiomyoma formation. The method comprises increasing the level of Cyr61 in leiomyoma tissue. The invention also describes compounds and compositions that stimulate induction of the Cyr61 gene and compounds that increase Cyr61 activity. The compositions and the method of the invention are useful for the preventing uterine leiomyoma formation or inhibiting proliferation of the cyr61 gene and compounds that increase Cyr61 activity. The preventing uterine leiomyoma formation or inhibiting proliferation of the cyr61 gene and compound in a particularly useful for treating or preventing uterine leiomyoma formation, or inhibiting proliferation of the cyr61 gene method is particularly useful for treating or preventing uterine leiomyoma formation, or inhibiting proliferation of uterine leiomyoma in a subject. The present sequence is sequence or represents by the sequence shown in Fig 6 is not shown in the correct sequence order in the figures. The start of the sequence is shown on page 8/10 of the figures and the rest of the sequence is shown on the cyrest of 
                                                                                                                                                                                                                                                                                                                                                                                                  Preventing uterine leiomyoma formation or inhibiting proliferation of uterine leiomyoma in subject, comprises modulating or increasing the level of Cyr61 in leiomyoma tissue .
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                                  /note= "
239..244
                                                         /note=
223..2
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202..2
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164..176
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145..150
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59..75
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47..51
            /note=
250..25
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Protein;
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                                                                                                                                                                                                                                                                                                                                              connective tissue
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                                                                                                                                                                                                                                                                                     liver failure; tranquillizer; tropic; hepatotropic; ulcer;
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             a mammal. The method comprises administering a polynucleotide encoding connective tissue growth factor-2 (CTGF-2) or an active fragment or its derivative. The method is useful for stimulating angiogenesis in a mammu preferably human having ischaemia or restenosis or is treated for limb revascularisation which is leg or arm. The invention is useful for treascularisation which is leg or arm. The invention is useful for the contraction of the contra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ulcer, etc), ag
liver failure),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          inhibiting tumour growth, where angiogenesis is utilised for enhancing the repair of connective and support tissue, promoting the attachment, fixation and stabilisation of tissue implants and enhancing wound healing, hence is useful for treating cardiovascular disease e.g. atherosclerosis, reperfusion injury such as heart failure, angina, ischaemia; and is also used to differentiate, proliferate and attract cells leading to regeneration of tissues which is utilised to repair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        administering connective nolvnucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Stimulating angiogenesis in a mammal preferably human having ischemia or restenosis or is treated for limb revascularization, by administering connective tissue growth factor-2 polypeptide or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
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18-MAY-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 e or protect tissue damaged by congenital defects, trauma (burns, etc), age, disease (e.g. osteoporosis, periodontal disease, failure), surgery including cosmetic plastic surgery. The present ce is human CTGF-2. CTGF-2 gene is useful in gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Adams
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                                                                  CTCIDGAVGCIPLCPQELSLPNLGCPNPRLVKVTGQCCEEWVCDEDSIKDPMEDQDGLLG
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                                                                                                                                                                                                                                                                                                                                                                         Conservative
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Pred. No. 1.2e
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                                 The present invention describes a method for the prevention or inhibition CC of breast cancer cell proliferation. The method comprises administration CC of a compound that inhibits the interaction of a sex steroid receptor with a sex steroid response element of the Cyr61 (cysteine rich heparin-CC which neutralises Cyr61 can be used to prevent or inhibit breast cancer CC cell proliferation by blocking sex steroid induced and growth factor induced synthesis of Cyr61 DNA, where the growth factor is epidermal, CC heparin binding epidermal or basic fibroblastic growth factor. (I) can be used to diagnose or stage breast cancer where the level of Cyr61 in a CC positive/suspect breast cancer cell is compared to the level in a CC normal tissue indicates the presence of breast cancer. The level of Cyr61 being determined by exposing the tissues to (I), and an increase in the level of breast cancer where the level of Cyr61 being determined by exposing the tissues to (I), and an increase in the level of cyr61 being determined by exposing the tissues to (I), and an increase in the level of cyr61 being determined by exposing the tissues to (I), and an increase in the level of cyr61 being determined by exposing the tissues to (I), and an increase in the level of cyr61 being determined by exposing the tissues to (I) and an increase in the level of cyr61 being determined by exposing the tissues to (I) and an increase in the level of cyr61 being determined by exposing the tissues to (I) and an increase in the level of cyr61 being determined by exposing the tissues to (I) and an increase in the level of cyr61 being determined by exposing the tissues to (I) and an increase in the level of cyr61 being determined by exposing the tissues to (I) and an increase in the level of cyr61 being determined by exposing the tissues to (I) and an increase in the level of cyr61 being the determined by exposing the tissues to (I) and an increase in the level of cyr61 being the determined by exposing the determined by exposing the determined by exp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 6; Fig 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Regulation of Cyr61 expression and activity for preventing and inhibiting breast cancer comprises use of a Cyr61 neutralizing antibody, an anti-sense oligonucleotide and an antibody which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB;
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16-MAY-2001;
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DB; ABA93127, ABA93130
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2001US-291510P
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Sequence

381

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Best Local S
Matches 379
                                                                                                                                                                                                               uraginosis; cytostatic; proliferative; vulnerary; immunomodulator; antidiabetic; antiasthmatic; antirheumatic; antiarthritic; antiviral; antiinflammatory; antithyroid; antiallergic; antibacterial; cardiant; dermatological; neuroprotective; thrombolytic concentrations.
                         N-PSDB;
useful for treating
         Novel
                                                   Rosen
                                                                                                     08-MAR-2000;
                                                                                                                                                                              dermatological; neuroprotective; thrombolytic; coagulant; nootropic; vasotropic; antipsoriatic; antiangiogenic; gene therapy; inflammation; immune disorder; haematopoletic cell disorder; autoimmune disorder; allergic reaction; graft versus host disease; organ rejection; haematopoletic; cardiovascular disorder; infection;
                                                                                     12-MAR-1999;
                                                                                                                      21-SEP-2000
                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                    Human; cancer
                                                                                                                                                                                                                                                                   Human cancer associated protein sequence
                                                                                                                                                                                                                                                                                     08-FEB-2001
                                                                                                                                                                                                                                                                                                      AAB43987;
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                         2000-587533/55
DB; AAC78196.
isolated nucleic
l for treating or
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                                                   CA,
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                                                                    HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NEDCSKTQPCDHTKGLECNFGASSTALKGICRAQSEGRPCEYNSRIYQNGESFQPNCQHQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MSSRIARALALVVTLLHLTRLALSTCPAACHCPLEAPKCAPGVGLVRDGCGCCKVCAKQL
                                                   Ruben
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                     2000WO-US05882
                                                                                                                                                                         thrombolytic; cardiovascular disease; drug screening.
                                                                                                                                                                                                                                                                                   (first entry)
                                                                    GENOME
                                                                                                                                                                                                                                                  associated gene; cancer antigen; detection;
                                                                                   99US-0124270.
                                                   MS
                                                                                                                                                                                                                                                                                                                     Protein;
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99.5%;
                                                                    SCI INC
                                                                                                                                                                        drug screening.
acids comprising diagnosing e.g. (
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Pred. No. 1
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cancer -
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1.2e-161;
                                                                                                                                                                                                                                                                   SEQ ID NO:1432.
        encoding peptides
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Best Local :
                                                                                   ABG76937
                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
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CC laim 11; Page 2116-2118; 2352pp; English.

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AAC77607 to AAC78448 encode the human cancer associated proteins given CC in AAA43398 to AAB44239. The proteins can have activities based on the CC tissues and cells the genes are expressed in. Example of activities CC include: cytostatic; proliferative; vulnerary; immunomodulator; CC antidiabetic; antishmatic; antishmatic; antiarthritic; coaquiant; CC antidiabetic; antishmatic; antishmatic; antiarthritic; coaquiant; CC dermatological; neuroprotective; cardiant; thrombolytic; coaquiant; CC dermatological; neuroprotective; cardiant; thrombolytic; coaquiant; CC mootropic; vasotropic; antipsoriatic and antiangiogenic. The CC polynucleotides and polypeptides can be used for preventing, treating or CC ameliorating medical conditions and diagnosing pathological conditions. CC polynucleotides, polypeptides, antibodies, agonists and antagonists from CC immune cells, to treat disorders of haematopoietic cells, autoimmune CC disorders, allergic reactions, graft versus host disease and organ CC inflammation, cancers, cardiovascular disorders, neurological disease and CC inflammation, cancers, cardiovascular disorders, neurological disease and CC cancerial or viral infections. The peptides, nucleotides, antibodies, agonists and antagonists may be also be used in the exemplification of CC the present invention.

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Sequence 455 AA;
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99.5%;

Score 2106; DB 21; Pred. No. 1.5e-161;

Length

455;

1 MSSRIARALALVVTLLHLTRLALSTCPAACHCPLEAPKCAPGVGLVRDGCGCCKVCAKQL HANEAAFPFYRLFNDIHKFRD 381 AGCLSVKKYRPKYCGSCVDGRCCTPQLTRTVKMRFRCEDGETFSKNVMMIQSCKCNYNCP KTCGTGISTRVTNDNPECRLVKETRICEVRPCGQPVYSSLKKGKKCSKTKKSPEPVRFTY KELGFDASEVELTRNNELIAVGKGRSLKRLPVFGMEPRILYNPLQGQKCIVQTTSWSQCS CTCIDGAVGCIPLCPQELSLPNLGCPNPRLVKVTGQCCEEWVCDEDSIKDPMEDQDGLLG CTCIDGAVGCIPLCPQELSLPNLGCPNPRLVKYTGQCCEEWVCDEDSIKDPMEDQDG1LG AGCLSVKKYRPKYCGSCVDGRCCTPQLTRTVKMRFRCEDGETFSKNVMMIQSCKCNYNCP ${\tt MSSRIARALALVVTLLHLTRLALSTCPAACHCPLEAPKCAPGVGLVRDGCGCCKVCAKQL}$ KTCGTGISTRVTNDNPECRLVKETRICEVRPCGQPVYSSLKKGKKCSKTKKSPEPVRFTY KELGFDASEVELTRNNELIAVGKGSSLKRLPVFGMEPRILYNPLQGQKCIVQTTSWSQCS Conservative 1; 455 Mismatches Indels 0; Gaps 360 434 300 180 194 120 134 60 374 314 240 254 0

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polypeptide, for treating or preventing a Novx-associated disorder (NoVI-8) and as a pharmaceutical composition comprising the polypeptide, copolynucleotide or the antibody. The polypeptides and polynucleotides are useful in diagnostic applications where their amounts are assessed, or for the manufacture of a medicament (e.g. gene therapy) for treating or preventing disorders or syndromes such as developmental disorders, immune diseases, signal transduction pathway disorders, metabolic disorders, feeding disorders (including obesity), wasting disorders, neurodegenerative disorders (including Alzheimer's disease and parkinson's disease), behavioural disorders, altergies, asthma, atheroselerosis, cardiomyopathy, angina pectoris, autoimmune disease, crithosis, diabetes, infectious disease (bacterial, fungal, protozoal and viral e.g. human immunodeficiency virus, HIV), cancer (e.g. prostate cancer), hypertension, hypotension, multiple sclerosis, urinary retention, osteoporosis, Crohn's disease, ulcers, may also be used as immunoders (e.g. anxiety), haemophilia or cirrhosis. They
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention discloses the isolated human polypeptides, and polypucleotides encoding them, that have been designated SECX and NOV. The polypeptides can be used for treating, or delaying, the onset of any logenic-associated disorder or treating a pathological state in a subject, preferably a mammal. They can also be used in determining the presence of, or predisposition to, a disease associated with altered levels of the polypeptides and polynucleotides of any one of the 12 sequences (SEC1-12), for raising antibodies, for identifying an agent that binds to, or that modulates the expression or activity of the
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Spytek KA,
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17-AUG-2001;
10-SEP-2001;
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11-JAN-2001;
11-JAN-2001;
11-JAN-2001;
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may also be used as immunogens to produce antibodies specific for the invention, and as vaccines. Further, they are useful for screening potential agonist and antagonist compounds. The sequences presented in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human SECX/NOVX polypeptide useful for diagnosing, preventing or treating disorders associated with aberrant expression or activity SECX/NOVX nucleic acids and proteins e.g., diabetes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                signal transduction pathway disorder; metabolic disorder; feeding disorder; obesity; wasting disorder; neurodegenerative disorder; feeding disorder; allergy;
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Casman SJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example
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)B; ABS59522.
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, Edinger S;
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Boldog F, Shimkets RA, Gorman L, Cr
Martin GB, Eisen A, Spaderna SK, V
Dipippo VA, Zerhusen BD, Peyman JA,
Grosse WM, Alsobrook JP, Lepley DM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; 2001US-261018P.
; 2001US-261026P.
; 2001US-261029P.
; 2001US-313170P.
; 2001US-318410P.
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2001US-261014P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MacDougall JR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                , Crasta OR, Mys
K, Vernet CAM, B
JA, Ellerman K;
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Best Local S
Matches 377
                                                                                                                                                                                                                          Human; suc-
gene therapy; musc-
+issue regeneration; a
                                                                                                 (HAST/)
(ADAM/)
                   growth factor, osteoporosis -
                                      Novel isolated
                                                          WPI; 2002-382150/41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                              Hastings GA,
                                                                                                                                 01-APR-1998;
                                                                                                                                         06-JUN-1995;
                                                                                                                                                             14-MAY-2001; 2001US-0853625
                                                                                                                                                                                                     US2002049304-A1
                                                                                                                                                                                                                         Unidentified
                                                                                                                                                                                                                                                                                    HCGF CNN family protein sequence
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                                                                                                                                                                                                                                                     small CCN-like growth factor;
herapy; muscle wasting disease;
                                                                                                 HASTINGS G
ADAMS M D.
                                                                                                                                                                                                                                                                                                                                                standard;
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                                                                              Adams
                            polynucleotide useful for trea
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98US-0053587
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                           treating musc
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Pred. No. 5
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                              muscle
                                                                                                                                                                                                                                                      SCGF; vulnerary; osteopathic;
; osteoporosis; wound healing;
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                                       encoding
                                                                                                                                                                                                                                                                                    NO:12
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.4e-161;
                             coding a wasting
                              disease,
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                                        small CCN-like
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Disclosure;

Fig

2A-D;

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RESULT 11
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Best Local
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                                                                                                                 Key
                                                                                                                                                                                                                                               25-MAR-2003
25-JUN-1996
            25-JAN-1996
                                                                            Protein
                                                                                                  Peptide
                                                                                                                                          Homo sapiens
                                                                                                                                                                                 cartilagenous
                                                                                                                                                                                             CTGF-2;
                                                                                                                                                                                                                      Connective
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                                    WO9601896-A1
                                                                                                                                                                    insulin-like
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                                                                                                                                                                                                                    tissue growth factor-2.
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                                                                                                                                                                s growth; skeletal; embryo; cell growth; morphogenesis; growth factor; fibroblast growth factor; Cry61.
                                                                                                                                                                                                                                           (updated)
(first entry)
                                                           1..24
/label= signal_peptide
25..375
/label= mature_protein
                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                            Protein;
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                                                                                                                                                                            ssue growth factor-2; secreted protein;
skeletal; embryo; cell growth; morphog
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RESULT 12
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Best Local
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N-PSDB; AAT12653.
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95.7%;
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   support tissue and can therefore treat skin disorders e.g., acne, UV damage or burns. CTGF-2 can be used to promote the attachment, fixation and stabilization of tissue implants inserted during reconstructive surgery, and can be used to enhance the healing of external wounds. It can be used in the treatment of injured or dependence in the promotes the growth of connective tissue, bone and ceme and the statement of the promotes of the growth of connective tissue, bone and ceme and the statement of the growth of connective tissue, bone and ceme and the statement of the growth of connective tissue, bone and ceme and the statement of the growth of connective tissue, bone and ceme and the statement of the statement 
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12-JUL-1994;
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F-2). CTGF-2 cDNA was isolated from a cDNA library derived
n foetal lung. In one instance, the cDNA was cloned into a
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                                                                                                                         MSSRIVRELALVVTLLHLTRVGLSTCPADCHCPLEAPKCAPGVGLVRDGCGCCKVCAKQL
NEDCRKTQPCDHTKGLECNFGASSTALKGICRAQSEGRPCEYNSRIYQNGESFQPNCKHQ
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                                                                                                           Stimulating angiogenesis in a mammal preferably human having ischemia or restenosis or is treated for limb revascularization, by administering connective tissue growth factor-2 polypeptide or polynucleotide
                                                                                                                                                                                                                                                                                                                                                                      Human; angiogenesis; connective tissue growth factor-2; CTGF-2; tumour; ischaemia; restenosis; tissue repair; wound healing; congenital defect; cardiovascular disease; atherosclerosis; heart failure; angina; trauma; burns; osteoporosis; periodontal disease; liver failure; tranquillizer; vulnerary; cosmetic plastic surgery; vasotropic; hepatotropic; ulcer; vulnerary;
                                                                                                                                                                         WPI;
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                                                                                                                                                              N-PSDB;
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18-MAY-2001;
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The present invention relates to a method for stimulating angiogenesis in a mammal. The method comprises administering a polynucleotide encoding connective tissue growth factor-2 (CTGF-2) or an active fragment or its derivative. The method is useful for stimulating angiogenesis in a mammal preferably human having ischaemia or restenosis or is treated for limb revascularisation which is leg or arm. The invention is useful for inhibiting tumour growth, where angiogenesis is utilised for enhancing the repair of connective and support tissue, promoting the attachment,

Disclosure;

Fig

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                                    18-JAN-1991;
10-JAN-1992;
                                                                                                      22-JUL-1992
                                                                                                                              EP495674-A2
                                                                                                                                                        Mus musculus
                                                                                                                                                                                embryo;
                                                                                                                                                                                            Transforming
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18-JAN-1993
          (BRIM ) BRISTOL-MYERS
                                                                           17-JAN-1992;
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                                                                                                                                                                             rming growth factor beta; induced; CEF-10;
fibroblasts; TGF-beta.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MSSRIARALALVYTLLHLTRLALSTCPAACHCPLEAPKCAPGVGLVRDGCGCCKVCAKQL
                                                                                                                                                                                                                                                                                                                                                                                                      PHANEAAFPFYRLF 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SKTCGTGISTRVTNDNPECRLVKETRICEVRPCGQPVYSSLKKGKKCSKTKKSPEPVRFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GKELGFDASEVELTRNNELIAVGKGRSLKRLPVFGMEPRILYNPLQGQKCIVQTTSWSQC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NEDCRKTQPCDHTKGLECNFGASSTALKGICRAQSEGRPCEYNSRIYQNGESFQPNCKHQ
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92US-0816270
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95.7%;
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             င္ပ
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Beta-IG-M2) contain 38 Dys residues and are induced by TGF-betal.

Beta-IG-M1 displays 80 percent homology to the CEF-10 protein

induced by v-src in chicken embryo fibroblasts and is identical

to the protein encoded by cyr61, an immediate early response gene

induced in quiescent BALB 3T3 cells by serum treatment. Residues

49-56 of beta-IG-M1 conform to the GCGCCXXC motif reported in the

amino half of insulin-like growth factor (IGF) binding proteins.

The C-terminal Cys rich region of beta-IG-M1, -M2 and CEF-10 contain

an amino acid sequence with strong homology to a motif found near the

C-terminal of the malarial circumsporozoite (CS) protein, which is

highly conserved among all species of malarial parasites sequenced

to date (designated region II). This motif is also found in

other proteins which have cell adhesive properties that mediate

cell-cell and cell-extracellular matrix interactions, such as

properdin, thrombospondin, and TRAP. The proteins encoded by

TGF-beta induced genes are likely to be involved in mediation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TGF-beta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the biological effects of TGF-beta relating to differentiation. See also AAR25566. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB;
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and differentiation effects of TGF-beta-1
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               CPHANEAAFPFYRLFNDIHKFRD 381
                                                                                     TYAGCLSVKKYRPKYCGSCVDGRCCTPQLTRTVKMRFRCEDGETFSKNVMMIQSCKCNYN
                                                                                                                                                      CSKTCGTGISTRVINDNPECRLVKETRICEVRPCGQPVYSSLKKGKKCSKTKKSPEPVRF
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CPHPNEASFRLYSLFNDIHKFRD
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                                                                                                                                                                                                                                                                                                                                                                                                            Fig 1; 35pp;
                                                                     TYAGCSSVKKYRPKYCGSCVDGRCCTPLQTRTVKMRFRCEDGEMFSKNVMMIQSCKCNYN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequence was deduced from the DNA sequence obtd.
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Pred. No. 2.3e-147;
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RESULT 15 AAE05920 ID AAE0

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Protein;

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Query Match
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Matches 348
                                                                                                                                                                protein (Fisp12) and connective tissue growth factor (CTGF) and nucleic acid molecules encoding such proteins. The polypeptides of the invention are members of cysteine-rich secreted protein family. Human Cyr61 fragment is useful in methods for screening modulators of cell adhesion, cell migration, fibroblast cell proliferation, angiogenesis, wound healing and Cyr61-integrin interaction. Modulator of Cyr61-integrin alphavbeta3 interaction is used for the preparation of a medicament for the fibrosis, tumour growth, disorders associated with inadequate angiogenesis; aberrant granulation tissue development; aberrant fibroblast growth and wounds. Polynucleotides of the invention are useful in gene therapy. The present sequence is mouse Cyr61
                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                    The invention relates to extracellular matrix (ECM) signalling molecules involved in cellular response to growth factors. More particularly the invention is directed to cysteine-rich protein (Cyr61), and Cyr61-related proteins such as fibroblast secreted (Cyr61).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel human cysteine-rich protein 61 (Cyr61) fragment useful in methods for screening for modulators of cell adhesion, fibroblast cell proliferation, angiogenesis and cell migration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31-JAN-2000; 2000US-0495448
15-MAY-2000; 2000US-0204364
06-OCT-2000; 2000US-0238705
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 1; Fig 1; 186pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB;
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MSSRIARALALVYTLLHLTRLALSTCPAACHCPLEAPKCAPGVGLVRDGCGCCKVCAKQL 60
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2.3e-147;
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                            CPHANEAAFPFYRLFNDIHKFRD
                                                                      TYAGCLSVKKYRPKYCGSCVDGRCCTPQLTRTVKMRFRCEDGETFSKNVMMIQSCKCNYN
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Search completed: August Job time: 40.1026 secs 'n 2003, 14:05:12

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                                                                                                                                                                                                                                                                                                                                                                                                                             /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
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/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/BCTUS_COMB.pep:*
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US-09-142-569-4
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US-09-142-569-4
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PATENT NO. 6413735

GENERAL INFORMATION:
APPLICANT: Lau, Lester F.
TITLE OF INVENTION: Extracellular Matrix Signalling Molecules
   Best Local Similarity
Matches 381; Conserv
                       Query Match
Best Local
                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/09/142,569
FILING DATE: 02-Apr-1999
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                               NAME/KEY: misc_feature
OTHER INFORMATION: "Human Cyr61 amino acid sequence"
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
                                                                                                                                                           FEATURE:
                                                                                                                                                                           TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                 TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: United
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: Illinois
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   100.0%; ilarity 100.0%; Conservative
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                                                                                                                                                                             protein
                                                                                                                                                                                                 linear
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     0;
                   Score 2116; DB 4;
Pred. No. 7.8e-177;
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ower, 233 South Wacker Drive
   Mismatches
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0;
                                       Length 381;
     Indels
     0;
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1 MSSRIARALALVVTLLHLTRLALSTCPAACHCPLEAPKCAPGVGLVRDGCGCCKVCAKQL 60

Gaps

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TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ
US-09-348-815-2
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US-09-348-815-2
                           Query Match
Best Local Similarity
Matches 379; Conserv
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                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/348,815
FILING DATE: 08-Jul-1999
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
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1 MSSRIARALALVVTLLHLTRLALSTCPAACHCPLEAPKCAPGVGLVRDGCGCCKVCAKQL 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AGCLSVKKYRPKYCGSCVDGRCCTPQLTRTVKMRFRCEDGETFSKNVMMIQSCKCNYNCP
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                                                                                                                                                                           TYPE: amino acid
                                                                                                                                                                                                                                                                                                       NAME: JONATHAN L. KLEIN REGISTRATION NUMBER: 41,119 REFERENCE/DOCKET NUMBER: PF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: ROCKVILLE STATE: MD
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TELEFAX: 301-309-8439
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                                                                                                                                                                                            LENGTH: 381 amino acids
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                                    Conservative
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                                                   99.5%;
                               Score 2106; DB 4;
Pred. No. 5.8e-176;
1: Mismatches 1;
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                                                                  Length 381;
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US-08-468-847B-12
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                                    US-08-468-847B-12
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Query Match
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                                                                                                                                                           TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO:
                                                   TOPOLOGY: L
                                                                                                                                          SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                TELECOMMUNICATION INFORMATION: TELEPHONE: 201-994-1700
                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: FILING DATE: 6 June
                                                                                 STRANDEDNESS:
                                                                                                                                                                                            TELEPHONE:
                                                                                                                                                                                                                                                   NAME: MULLINS, J.G. REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER:
                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: 3.5
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ADDRESSEE: CECCHI, STEWART & OLSTEIN
                                                                                                                      LENGTH:
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                                                                                                       AMINO ACID
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                                                                                                                         374 AMINO ACIDS
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                                                                    LINEAR
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                                                     PROTEIN
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93.2%;
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Human CCN-Like Growth
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Score 1971.5;
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US-08-459-101A-2
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                                                                                TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: LI, ET AL.
TITLE OF INVENTION: Connective Tissue Growth Factor-2
NUMBER OF SEQUENCES: 6
                                                                SEQUENCE CHARACTERISTICS:
                                                                                                                TELECOMMUNICATION INFORMATION: TELEPHONE: 201-994-1700
                                                                                                                                                                                                 FILING DATE: 12 JUL 94 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                              CLASSIFICATION: 536
PRIOR APPLICATION NUMBER: 1
                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/459,101A FILING DATE: June 2, 1995 CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
                                LENGTH: 375 AMINO ACIDS TYPE: AMINO ACID
                                                                                                                                               NAME: FERRARO, GREGORY D.
REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 325800-317
                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: ROSELAND
STATE: NEW JERSEY
                  STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
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ADDRESSEE: CECCHI, STEWART & OLSTEIN
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Best Local Similarity
Matches 357; Conser
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           TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 32
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INC
                                                                                                                                                                          APPLICATION NUMBER: US/01 FILING DATE: 6 June 1995 CLASSIFICATION: 435 PRIOR APPLICATION DATA:
SEQUENCE CHARACTERISTICS:
                                                                                                                            FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: HUNDMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
                                                                                                                                                                                                                                                                        COMPUTER: IBM PS,
OPERATING SYSTEM:
                                                                                             NAME: MULLINS, J.G. REGISTRATION NUMBER:
                                            TELEPHONE:
                                                                                                                                                                APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
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no. 5780263
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VENTION: Human CCN-Like Growth Factor
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Pred. No. 1.3e-163;
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US-09-142-569-2
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INFORMATION
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                                              NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 28758/33766
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
                                                                                                                                                                                           COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                              APPLICATION NUMBER: US/09/142,569
FILING DATE: 02-Apr-1999
CLASSIFICATION: <UDknown>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Extracellular Matrix Signalling Molecules NUMBER OF SEQUENCES: 17
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AMINO ACID
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                                                                                                                                                                                                                                                                                                                             CITY: Chicago
STATE: Illinois
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               TELEFAX: 312/474-0448
TELEX: 25-3856
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90.9%; Pred. No. 1.6e-160;
tive 10; Mismatches 19;
NO:
                                                                                                                                                                                                                                                                                                                                                            Tower,
                                                                                                                                                                                                                                                                                                                                                            , O'Toole, o
                                                                                                                                                                                                                                                                                                                                                            Gerstein, Murray & South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 379;
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                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-468-847B-13; Sequence 13, Application US/08468847B
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                                                                                                                                                                                                                                                                                                                                                                                                     Patent No. 5780263
GENERAL INFORMATION:
APPLICANT: Hastin
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
                                                                                                                                                                                                                        STREET: 0 L.
STREET: NOSELAND
CTATE: NEW JERSEY
MSA
ATTORNEY/AGENT
                                               PRIOR APPLICATION DATA:
                                                                                                             CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Human CCN-Like Growth NUMBER OF SEQUENCES: 20
                                                           APPLICATION NUMBER: US/ON APPLICATION NUMBER: US/ON FILLING DATE: 6 June 1995
               FILING DATE:
                             APPLICATION NUMBER:
                                                                                                                                SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
nes 348; Conserv
                                                                                                                                                                                                                                                                                                          ADDRESSEE:
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                                                                                                                                WORD PERFECT 5.1
                                                                                                                                                                                                                                                                                             CARELLA, BYRNE, BAIN, GIL CECCHI, STEWART & OLSTEIN
INFORMATION
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                                                                                               US/08/468,847B
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Pred. No. 1
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356

180 178 238 236 298

296

120

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; SEQ ID NO 2
; LENGTH: 347
; TYPE: PRT
; ORGANISM: Rat
US-09-582-337-2
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                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Japan Tobacco, Inc.
TITLE OF INVENTION: and Medicinal Uses Thereof
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                         Sequence 2, Application US/09582337 Patent No. 6562618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local (
                                                                                                                                                               CURRENT FILING DATE: 2000-06-23
PRIOR APPLICATION NUMBER: JP P1997-367699
PRIOR FILING DATE: 1997-12-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 375 AMINO ACIDS
TYPE: AMINO ACID
GENERALIZATION ACID
                                                                                                           NUMBER OF SEQ ID NOS: 27 SOFTWARE: PatentIn Ver.
                                                                                                                                    PRIOR APPLICATION NUMBER: JP P1998-356183
PRIOR FILING DATE: 1998-12-15
                                                                                                                                                                                                       FILE REFERENCE: J1-009PCT CURRENT APPLICATION NUMBER: US/09/582,337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 32: TELECOMMUNICATION INFORMATION: TELEPHONE: 201-994-1700
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MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QCSKTCGTGISTRVTNDNPECRLYKETRICEVRPCGQPYYSSLKKGKKCSKTKKSPEPVR 297
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45.0%;
46.2%;
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Score 953; DB 4; Pred. No. 2.2e-75;
            Length 347;
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; ORGANISM: Mouse
US-09-292-036-3
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US-09-292-036-3
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                                                                                                                                                                            Query Match
Best Local Similarity
Matches 178; Conserv
                                                                                                                                                                                                                                                                                         SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
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                                                                                                                                                                                                                                                                           LENGTH: 348
            120
                           118 QHQCTCIDGAVGCIPLCPQELSLPNLGCPNPRLVKVTGQCCEEWVCDEDSIKDPMEDQDG 177
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            KYQCTCLDGAVGCVPLCSMDVRLPSPDCPFPRRVKLPGKCCEEWVCDEP--
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Sequence 3, Application US/09292036 Patent No. 6358741
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: CONNECTIVE TISSUE GROWTH FACTOR (CTGF) AND METHODS FILE REFERENCE: FIBRO1100-1 CURRENT APPLICATION NUMBER: US/09/292,036

CURRENT FILING DATE: 1999-04-14
                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR FILING DATE: 1998-11-06
NUMBER OF SEQ ID NOS: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: US 09/292,036 PRIOR FILING DATE: 1999-04-14
                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: US 09/187,478
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QCSKTCGTGISTRVTNDNPECRLVKETRICEVRPCGQPVYSSLKKGKKCSKTKKSPEPVR
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                              KQLNEDCSKTQPCDHTKGLECNFGASSTALKGICRAQSEGRPCEYNSRIYQNGESFQPNC 117
                                                                                             MLASVAGPISLALVLLALCTRPATGQDCSAQCQCAAEAAPHCPAGVSLVLDGCGCCRVCA
                                                                                                                                          MSSRIARALALVVTLLHL-TRLAL-STCPAACHCPLE-APKCAPGVGLVRDGCGCCKVCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FTYAGCLSVKKYRPKYCGSCVDGRCCTPQLTRTVKMRFRCEDGETFSKNVMMIQSCKCNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACSKTCGMGISTRVTNDNTFCRLEKQSRLCMVRPCEADLEENIKKGKKCIRTPKIAKPVK
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  KQLGELCTERDPCDPHKGLFCDFGSPANRKIGVCTAK-DGAPCVFGGSVYRSGESFQSSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCPHANEAAFPFY--RLFNDI 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MLASVAGPVSLALVLLLCTRPATGQDCSAQCQCAREAAPRCPAGVSLVLDGCGCCRVCAK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CARMICHAEL, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ALLEN, Margaret SVERDRUP, Fran
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SCHMIDT, Brian
                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                       45.0%; Score 952.5; DB 4
46.6%; Pred. No. 2.5e-75;
7ative 57; Mismatches 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----KDRTVVGPALAAYRLEDTFGPDPTMM-----RANCLVQTTEWS
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                                                                                                                                                                                                                                       DB 4;
                                                                                                                                                                                            106;
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US-08-468-847B-15
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US-08-468-847B-15
                                                                                                                                                                Matches
                                                                                                                                                                             Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                  TOPOLOGY: LI
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 32
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: 3.5 INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Human CCN-Like NUMBER OF SEQUENCES: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PS/2
OPERATING SYSTEM: I
                                                                                                                                                                                                                                                                                   STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: MULLINS, J.G. REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                    LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
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                     61
                                                                                                                                                                             Similarity
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                                                                                                         MSSRIARALALVVTLLHL-TRLAL-STCPAACHCPLE-APKCAPGVGLVRDGCGCCKVCA 57
                                                                                                                                                                                                                                                                                                     AMINO ACID
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                                                      KQLNEDCSKTQPCDHTKGLECNFGASSTALKGICRAQSEGRPCEYNSRIYQNGESFQPNC 117
                  {\tt KQLGELCTERDPCDPHKGLFCDFGSPANRKIGVCTAK-DGAPCVFGGSVYRSGESFQSSC}
                                                                                     MLASVAGPISLALVILLALCTRPATGQDCSAQCQCAAEAAPHCPAGVSLVLDGCGCCRVCA
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E: CECCHI, STEWART
6 BECKER FARM ROAD
                                                                                                                                                                                                                                                                                                                    348 AMINO ACIDS
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                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                     LINEAR
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                                                                                                                                                                                                                                                  PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INCH DISKETTE
                                                                                                                                                                           44.8%; Score 948.5; DB 1
46.3%; Pred. No. 5.5e-75;
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                                                                                                                                                             Mismatches
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                                                                                                                                                                                             DB 1;
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                                                                                                                                                             106;
                                                                                                                                                                                            Length 348;
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                                                                     Matches
                                                                                     Query Match
Best Local
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                                                                                                                                                                                                                                                                                              TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 348 amino acids
                                                                                                                                                       NAME/KEY: misc_feature
OTHER INFORMATION: "Fisp12
SEQUENCE DESCRIPTION: SEQ ID NO: 6
                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY_AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36.
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                              FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
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                                                                     177; Conserv
                                  1 MSSRIARALALVVTLLHL-TRLAL-STCPAACHCPLE-APKCAPGVGLVRDGCGCCKVCA
MLASVAGPISLALVLLALCTRPATGQDCSAQCQCAAEAAPHCPAGVSLVLDGCGCCRVCA
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::||||:|||||||
KYQCTCLDGAVGCVPLCSMDVRLPSPDCPFPRRVKLPGKCCKEWVCDEP--------
                                                                                                                                                                                                                                               STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 02-Apr-1999 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YNCPGDNDIFESLYYRKMYGDM 347
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                                                                                                                                                                                                                                                                                 TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: United States of America ZIP: 60606-6402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KFELSGCTSVKTYRAKFCGVCTDGRCCTPHRTTTLPVEFKCPDGEIMKKNMMFIKTCACH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/09/142,569
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LLGKELGFDASEVELTRNNELIAVGKGRSLKRL-PVFGMEPRILYNPLQGQKCIVQTTSW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Marshall,
                                                                       Conservative
                                                                                                                                                                                                                                                                                 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6300 Sears Tower,
                                                                                                                                                                                                                              protein
                                                                                     44.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US/09142569
                                                                     Score 948.5; |
Pred. No. 5.5e
58; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         O'Toole, Gerstein, Murray & ower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                           36,107
                                                                                                                                                                                                                                                                                                                                                                                                                          28758/33766
                                                                                                                                                             6
                                                                                                                                                                           amino
                                                                                     5e-75;
                                                                                                        DB 4;
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; LENGTH: 347
; TYPE: PRT
; ORGANISM: NO. (
US-09-187-478-2
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US-09-187-478-2
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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APPLICANT: Allen, Margaret L.
TITLE OF INVENTION: Connective Tissue Growth (CTGF) And Methods
FILE REFERENCE: 08765/004001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/187,478 CURRENT FILING DATE: 1998-11-06
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                                      FTYAGCLSVKKYRPKYCGSCVDGRCCTPQLTRTVKMRFRCEDGETFSKNVMMIQSCKCNY 357
                                                                                                 QCSKTCGTGISTRVTNDNPECRLVKETRICEVRPCGQPVYSSLKKGKKCSKTKKSPEPVR 297
                                                                                                                                                                                                                                 HQCTCIDGAVGCIPLCPQELSLPNLGCPNPRLVKVTGQCCEEWVCDEDSIKDPMEDQDGL 178
                                                                                                                                                                                                                                                                            QLGELCTERDPCDPHKSLFCDFGSPANRKIGVCTAK-DGAPCVFGGSVYRSGESFQSSCK
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                  FELSGCTSVKTYRAKFCGVCTDGRCCTPHRTTTLPVEFKCPDGEIMKKNMMFIKTCACHY
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46.3%; Pred. No. 6e-75;
Live 58; Mismatches 1
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; TYPE: PRT
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US-09-292-036-2
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US-09-292-036-2
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US-08-167-628-2
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LENGTH: 347
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GENERAL INFORMATION:
APPLICANT: Grotendorst, Gary R.
APPLICANT: Bradham Jr., Douglas
TITLE OF INVENTION: CONNECTIVE
NUMBER OF SEQUENCES: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/292,036
CURRENT FILING DATE: 1999-04-14
PRIOR APPLICATION NUMBER: US 09/292,036
PRIOR FILING DATE: 1999-04-14
PRIOR APPLICATION NUMBER: US 09/187,478
PRIOR FILING DATE: 1998-11-06
NUMBER OF SEQ ID NOS: 18
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TITLE OF INVENTION: CONNECTIVE TISSUE GROWTH
FILE REFERENCE: FIBRO1100-1
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               Jr., Douglas M.,
CONNECTIVE TISSUE GROWTH FACTOR
                                                                                               US/08167628
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Pred. No. 6e-75;
8; Mismatches 1
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              Sequence 2, Application US/08386680 Patent No. 5585270 GENERAL INFORMATION:
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   APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Wetherell, Jr. Ph.D.,
REGISTRATION NUMBER: 31,678
REFERENCE/DOCKET NUMBER: PD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Spensley Horn Jubas & Lubitz
STREET: 4225 Executive Square, Suite 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: 619-455-5100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 349 amino acids TYPE: amino acid TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        h 44.8%; Score 947; DB Similarity 46.6%; Pred. No. 7.4e 74; Conservative 58; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Wetherell, Jr. Ph.
REGISTRATION NUMBER: 31,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 10-FEB-
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS: Cornessey Horn Jubas & Lubitz
ADDRESSEE: Spensley Horn Jubas & Lubitz
STREET: 4225 Executive Square, Suite 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Bradham Jr., Douglas M., TITLE OF INVENTION: CONNECTIVE TISSUE GROWTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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ilarity 46.6%;
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PRIOR APPLICATION NUMBER: 09/348 815
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PRIOR APPLICATION NUMBER: 08/459,101
PRIOR APPLICATION NUMBER: 08/459,101
PRIOR APPLICATION NUMBER: PCT/US94/07736
PRIOR FILING DATE: 1994-07-12
PRIOR APPLICATION NUMBER: 60/217,402
PRIOR FILING DATE: 2000-07-11
PRIOR FILING DATE: 2000-07-11
PRIOR FILING DATE: 2001-05-18
NUMBER OF SEO TO NUMBER: 60/291,642
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OTHER INFORMATION: "H
SEQUENCE DESCRIPTION: SEQ ID
US-10-053-753-4_
                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Li, Haodong
APPLICANT: Adams, Marl
APPLICANT: Calenda Va.
Query Match
Best Local Similarity
Matches 379; Conserv
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                                                                                                                                        SEQ ID NO 2
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Best Local
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TITLE OF INVENTION: Connective Tissue Growth
FILE REFERENCE: pF126P2
CURRENT APPLICATION NUMBER: US/09/901,910
CURRENT FILING DATE: 2001-07-11
                                                                                                                                                        SOFTWARE: PatentIn version 3.0
                                                                                                                        LENGTH:
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US-10-294-796-2
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SEQ ID NO 2
LENGTH: 381
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Best Local S
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PRIOR FILING DATE: 1995-06-02
PRIOR APPLICATION NUMBER: PCT/US94/07736
PRIOR FILING DATE: 1994-07-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/10/294,796
CURRENT FILING DATE: 2002-11-15
PRIOR APPLICATION NUMBER: US 09/348,815
PRIOR FILING DATE: 1999-07-08
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APPLICANT: Rosen et al.

TITLE OF INVENTION: Nucleic acids, Proteins and Antibodies
FILE REFERENCE: PA106
CURRENT APPLICATION NUMBER: US/09/925,301
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05882
PRIOR FILING DATE: 2000-03-08
PRIOR FILING DATE: 2000-03-08
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1694
SOFTMARE: Patentin Ver. 2.0
SEQ ID NO 1432
        RESULT 5
US-10-205-823-84
VS-10-205-823-84
Sequence 84, Application US/10205823
Publication No. US20030108963A1
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US-09-925-301-1432
    GENERAL INFORMATION:
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ilarity 99.5%;
Conservative
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Pred. No. 2.5e-172;
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; TYPE: PRT
; ORGANISM: Hom
US-10-205-823-84
RESULT 6
US-09-853-625B-12
; Sequence 12, Application U
; Patent No. US20020049304A1
; GENERAL INFORMATION:
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PRIOR FILING DATE: 2001-08-22
PRIOR APPLICATION NUMBER: 60/325,020
PRIOR FILING DATE: 2001-09-25
PRIOR APPLICATION NUMBER: 60/341,746
PRIOR FILING DATE: 2001-12-12
PRIOR APPLICATION NUMBER: 60/362,158
PRIOR FILING DATE: 2002-03-05
PRIOR FILING DATE: 2002-03-05
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Best Local Similarity
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APPLICANT:
APPLICANT:
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TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS,
TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASS
TITLE OF INVENTION: THERAPY OF PROSTATE CANCER
FILE REFERENCE: MRI-044
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Gorbatcheva, Bella
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Kamatkar, Shubhangi
Angela M.
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99.0%;
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Pred. No. 1
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HOLECULE TYPE: PROTEIN SEQUENCE DESCRIPTION: 909-853-625B-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Local 358;
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APPLICATION NUMBER: US/09/853,625B
FILING DATE: 14-May-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 II
COMPUTER: IBM PS/2
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NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA, BYRNE,
CECCHI, STEWART
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 325800-442
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
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PHANEAAFPFYRLF
                            PHANEAAFPFYRLF 373
                                                                  YAGCLSVKKYRPKYCGSCVDGRCCTPQLTRTVKMRFPCEDGETFSKNVMMIQSSKCNYNC
                                                                                  YAGCLSVKKYRPKYCGSCVDGRCCTPQLTRTVKMRFRCEDGETFSKNVMMIQSCKCNYNC
                                                                                                                                  SKTCGTGISTRVTNDNPECRLVKETRICEVRPCGQPVYSSLKKGKKCSKTKKSPEPVRFT
                                                                                                                                                    SKTCGTGISTRVTNDNPECRLVKETRICEVRPCGQPVYSSLKKGKKCSKTKKSPEPVRFT
                                                                                                                                                                                                    GKELGFDASEVELTRNNELIAVGKGRSLKRLPVFGMEPRILYNPLOGQKCIVQTTSWSQC
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                                                                                                                                                                                                                                                                                                                                            NEDCRKTQPCDHTKGLECNFGASSTALKGICRAQSEGRPCEYNSRIYQNGESFQPNCKHQ
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STREET: 6 BECKER FARM
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; ORGANISM: homo
US-09-901-910-7
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                                                                                                                                                      RESULT
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US-09-901-910-7
                                                                              Sequence 11, Application US/09853625B Patent No. US20020049304A1 GENERAL INFORMATION:
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Best Local :
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SEQ ID NO 7
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PRIOR ADDITORMENT 1999-07-08

PRIOR ADDITORMENT 1999-07-08
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/901,910 CURRENT FILING DATE: 2001-07-11
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TITLE OF INVENTION: Connective Tissue Growth Factor-2
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CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA,
                              APPLICANT: Hastings, Gregg
TITLE OF INVENTION: Human C
NUMBER OF SEQUENCES: 20
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                                                                                                                                                                                                                                                                           YAGCLSVKKYRPKYCGSCVDGRCCTPQLTRTVKMRFPCEDGETFSKNVMMIQSSKCNYNC
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                                                  g A. and Adams, N
CCN-Like Growth
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300 299 240

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TOPOLOGY: LINEAR
; MOLECULE TYPE: PROTEIN
; SEQUENCE DESCRIPTION: SEQ ID
US-09-853-625B-11
RESULT 9
US-10-053-753-2
; Sequence 2, Application US/10053753
; Publication No. US20020150986A1
; GENERAL INFORMATION:
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TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 11:
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APPLICATION NUMBER: 09/053,587
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: MULLINS, J.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
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MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
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                                                                                                                       CPHPNEASFRLYSLFNDIHKFRD
                                                                                                                                             CPHANEAAFPFYRLFNDIHKFRD 381
                                                                                                                                                                                                                                                          CSKTCGTGISTRVTNDNPECRLVKETRICEVRPCGQPVYSSLKKGKKCSKTKKSPEPVRF 298
                                                                                                                                                                                                                                                                                                                                                                                                                    CTCIDGAVGCIPLCPQELSLPNLGCPNPRLVKVTGQCCEEWVCDEDSIKDPMEDQDGLLG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/09/853,625B FILING DATE: 14-May-2001 CLASSIFICATION: <Unknown>
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CITY: ROSELAND
STATE: NEW JERSEY
COUNTRY: USA
                                                                                                                                                                                          TYAGCSSYKKYRPKYCGSCVDGRCCTPLQTRTVKMRFRCEDGEMFSKNVMMIQSCKCNYN
                                                                                                                                                                                                                                                                                                                                                                                                CTCIDGAVGCIPLCPQELSLPNLGCPNPRLVKVSGQCCEEWVCDEDSIKDSLDDQDDL--
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90.9%;
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Pred. No. 2.9e-157;
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OTHER INFORMATION: "Mouse Cyr61 amino acid sequence";
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-053-753-2
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
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FILING DATE: 22-Jan-2002
CLASSIFICATION: <UNknown>
ATTORNEY/AGENT INFORMATION:
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TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
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                                                                                                                                                                                                                                                          181 KELGFDASEVELTRNNELIAVGKGRSLKRLPVFGMEPRILYNPL--QGQKCIVQTTSWSQ 238
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                                                     CPHPNEASFRLYSLFNDIHKFRD
                                                                         CPHANEAAFPFYRLFNDIHKFRD 381
                                                                                                                                         TYAGCLSVKKYRPKYCGSCVDGRCCTPQLTRTVKMRFRCEDGETFSKNVMMIQSCKCNYN
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                                                                                                                       TYAGCSSVKKYRPKYCGSCVDGRCCTPLQTRTVKMRFRCEDGEMFSKNVMMIQSCKCNYN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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MOLECULE TYPE: PROTEIN

SEQUENCE DESCRIPTION: 02-09-853-625B-13
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: 3.5 INCH DISKE COMPUTER: IBM PS/2 OPERATING SYSTEM: MS-DOS SOFTWARE: WORD PERFECT 5.1 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: MULLINS, J.G.
REGISTRATION NUMBER: 33,073
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: <Unknown> PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 07068
COMPUTER READABLE FORM:
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 NCPHANEAAFPFYRLFNDIHKFRD 381
                                                      FTYAGCLSVKKYRPKYCGSCVDGRCCTPQLTRTVKMRFRCEDGETFSKNVMMIQSCKCNY
                                                                                                    QCSKTCGTGISTRYTNDNPDCKLIKETRICEVRPCGQPSYASLKKGKKCTKTKKSPSPVR
                                                                                                                    QCSKTCGTGISTRYINDNPECRLVKETRICEVRPCGQPYYSSLKKGKKCSKTKKSPEPVR
                                                                                                                                                                                       GKELGFDASEVELTRNNELTAVGKGRSLKRLPVFGMEP--RILINPLQGQKCIVQTTSWS 237
                                                                                                                                                                                                                                                           QCTCIDGAVGCIPLCPQELSLPNLGCPNPRLVKVTGQCCEEWVCDEDSIKDPMEDQDGLL 179
                                                                                                                                                                                                                                                                                                            LNEDCSRTQPCDHTKGLECNFGASPAATNGICRAQSEGRPCEYNSKIYQNGESFQPNCKH 119
                                                                                                                                                                                                                                                                                                                                            LNEDCSKTQPCDHTKGLECNFGASSTALKGICRAQSEGRPCEYNSRIYQNGESFQPNCQH 119
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                                                                                                                                                                      SKEFGLDASEGELTRNNELIAIVKG-GLKMLPVFGSEPQSRAFENP----KCIVQTTSWS
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CECCHI, STEWART
STREET: 6 BECKER FARM ROAD
CITY: ROSELAND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 201-994-1744
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0; Mismatches
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Pred. No. 3.2e-137;
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RESULT 11
US-10-245-977-7
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SEQ ID NO 7
                                                                                                             APPLICANT: FIBROGEN, I
APPLICANT: SCHMIDT, B
APPLICANT: ALLEN, Mar
APPLICANT: SVENDRUP,
                                                                                                                                                                                                                Sequence 3, Application US/10101040 Publication No. US20020142353A1
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                                                                                                                                                                                         GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                      APPLICANT: CARMICHAEL, David
TITLE OF INVENTION: CONNECTIVE TISSUE GROWTH FACTOR (CTGF)
TITLE OF INVENTION: USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT FILING DATE: 2002-09-18
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TITLE OF INVENTION: METHODS OF
FILE REFERENCE: FP0812 US
FILE REFERENCE: FIBRO1100-1
CURRENT APPLICATION NUMBER: US/10/101,040
CURRENT FILING DATE: 2002-03-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Weitz, Stephen L APPLICANT: Usinger, William
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TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QLNEDCSKTQPCDHTKGLECNFGASSTALKGICRAQSEGRPCEYNSRIYQNGESFQPNCQ 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LGKELGFDASEVELTRNNELIAVGKGRSLKRL-PVFGMEPRILYNPLQGQKCIVQTTSWS
                                                                                                                 ALLEN, Margaret SVERDRUP, Fran
                                                                                                                                                       SCHMIDT, Brian
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46.2%;
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Pred. No. 6.9e-74;
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RESULT 13
US-09-853-625B-15
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                                                                                                                                                                                                                                                                                                                                         Sequence 15, Application US/09853625B Patent No. US20020049304A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 178;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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NUMBER OF SEQ ID NOS: 18
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                                                            ZIP: 07068

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETT
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local
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APPLICATION NUMBER: US 09/292,036
FILING DATE: 1999-04-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 09/292,036
   PRIOR
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                                                                                                                                                                                                                                                                                          APPLICANT: Hastings, Gregorithm OF INVENTION: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      266
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KPELSGCTSVKTYRAKFCGVCTDGRCCTPHRTTTLPVEFKCPDGEIMKKNMMFIKTCACH
                               APPLICATION NUMBER: US/09/853,625B FILING DATE: 14-May-2001
                                                                                                                                                                                             CITY: ROSELAND
STATE: NEW JERSEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YNCPHANEAAFPFY--RLFNDI 376
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                CLASSIFICATION:
                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                             STREET: 6 BECKER FARM ROAD
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   APPLICATION DATA:
                                                                                                                                                                                                                                                            ADDRESSEE: CARELLA, BYRNE,
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Human CCN-Like
                                                                                                                               INCH DISKETTE
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Pred. No. 1.1
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e Growth Fact
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US-10-053-753-6
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                                                                                                                                                                                                                                                                         Sequence 6, Application US/10053753 Publication No. US20020150986A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity Matches 177; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Lau, Lester F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1740
TELEPAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CURRENT APPLICATION DATA:
                                                                                                                                                                                          CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: PROTEIN SEQ ID NO: 15:
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NAME: MULLINS, J.G.
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             COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0
                                                                                                                          STREET: 6300 Sears Tower,
CITY: Chicago
STATE: Illinois
                                                                                                                                                                                                                                                                                                                                                                         YNCPGDNDIFESLYYRKMYGDM
                                                                                                                                                                                                                                                                                                                                                                                                     YNCPHANEAAFPFY--RLFNDI 376
                                                                                            COUNTRY: United States of America ZIP: 60606-6402
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 09/053,587 FILING DATE: <Unknown>
                                                                                                                                                            ADDRESSEE: Marshall, O'Toole, STREET: 6300 Sears Tower, 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: LINEAR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER: 33,073
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                #1.0,
               Version #1
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MSSRIARALALVVTLLHL-TRLAL-STCPAACHCPLE-APKCAPGVGLVRDGCGCCKVCA
MLASVAGPISLALVILALCTRPATGQDCSAQCQCAAEAAPHCPAGVSLVLDGCGCCRVCA
                                                                                                             DB 9;
                                                                            106;
                                                                          Indels
                                                                                                             Length 348;
                                                                          41;
                                                                          Gaps
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8

TITLE OF INVENTION: Extracellular Matrix Signalling Molecules NUMBER OF SEQUENCES: 17 **YQCTCLDGAVGCVPLCSMDVRLPSPDCPFPRRVKLPGKCCKEWVCDEP--KFELSGCTSVKTYRAKFCGVCTDGRCCTPHRTTTLPVEFKCPDGEIMKKNMMFIKTCACH QHQCTCIDGAVGCIPLCPQELSLPNLGCPNPRLVKVTGQCCEEWVCDEDSIKDPMEDQDG 177 KQLNEDCSKTQPCDHTKGLECNFGASSTALKGICRAQSEGRPCEYNSRIYQNGESFQPNC 117 RFTYAGCLSVKKYRPKYCGSCVDGRCCTPQLTRTVKMRFRCEDGETFSKNVMMIQSCKCN 356 SACSKTCGMGISTRVTNDNTFCRLEKQSRLCMVRPCEADLEENIKKGKKCIRTPKIAKPV SQCSKTCGTGISTRVTNDNPECRLVKETRICEVRPCGQPVYSSLKKGKKCSKTKKSPEPV 296 LIGKELGFDASEVELTRNNELIAVGKGRSLKRL-PVFGMEPRILYNPLQGQKCIVQTTSW 236 KQLGELCTERDPCDPHKGLFCDFGSPANRKIGVCTAK · DGAPCVFGGSVYRSGESFQSSC -----KDRTAVGPALAAYRLEDTFGPDPTMM-----RANCLVQTTEW Gerstein, Murray & South Wacker Drive 325 265 205 168 119

. 30

CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:

APPLICATION NUMBER: US/10/053,753 FILING DATE: 22-Jan-2002

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NAME/KEY: misc_feature;
OTHER INFORMATION: "Fispl2;
SEQUENCE DESCRIPTION: SEQ ID NO: 6
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                                                                                                                                                                                                         Sequence 8, Application US/10245977 Publication No. US20030113816A1 GENERAL INFORMATION:
SOFTWARE:
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Best Local :
                                                 CURRENT APPLICATION NUMBER: US/10/245,977
CURRENT FILING DATE: 2002-09-18
PRIOR APPLICATION NUMBER: US 60/323,305
PRIOR FILING DATE: 2001-09-18
                                                                                                                              APPLICANT: Weitz, Stephen L
APPLICANT: Usinger, William R
TITLE OF INVENTION: METHODS OF ASSAYING CONNECTIVE TISSUE GROWTH FACTOR
FILE REFERENCE: FP0812 US
                                     NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 348 amino acids
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TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein
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177; Conserv
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                 PatentIn version 3.1
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                                                                                                                                                                                                                                                                                                                                             YNCPGDNDIFESLYYRKMYGDM 347
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REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 28
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Pred. No. 2.5e-73;
8; Mismatches 106;
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326
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Pred. No. 2.5e-73;
8; Mismatches 106;
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Search completed: August 5, 2003, 14:18:51 Job time: 35.5908 secs

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Minimum DB
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Maximum Match 100%
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                                                                                                                       notch4 - mouse
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beta IG-M2 protein
connective tissue
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                                                  - bovin
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45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30
132	132	132	132	132	132.5	133	133.5	134	134	134	134	134.5	134.5	135	135
6.2	6.2	6.2	6.2	6.2	6.3	6.3	6.3	6.3	6.3	6.3	6.3	6.4	6.4	6.4	6.4
2823	2823	1531	1469	251	2555	2813	1955	3704	3672	3106	1959	4006	330	1170	1168
N	N	N	N	ν	N	1	ᆫ	N	N	Ĺ	Н	N	N	N	N
F87908	T23064	T42218	в36665	A55035	A40043	UHWV	AGCH	T37316	T23433	S53868	AGRT	T09070	T25169	A40558	I56985
protein T22A3.8 [i	hypothetical prote	slit-1 protein hom	slit protein 2 pre	cysteine-rich prot	notch protein homo	von Willebrand fac	agrin precursor -	probable laminin a	hypothetical prote	laminin alpha-2 ch	agrin - rat	probable tenascin	hypothetical prote	thrombospondin 1 p	kalinin Bl - mouse

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gene CYR61 protein precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 28-Sep-1990 #sequence_revision 18-Nov-1992 #text_change 05-Nov-1999
C;Accession: A35669; I48319; S16446
R;O'Brien, T.P.; Yang, G.P.; Sanders, L.; Lau, L.F.
Mol. Cell. Biol. 10, 3569-3577, 1990
A;Title: Expression of cyr61, a growth factor-inducible immediate-early general procession of cyr61, a growth factor-inducible immediate-
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C;Superfamily: von Willebrand factor type C repeat homology
F;99-166/Domain: von Willebrand factor type C repeat homology <VWC>
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A; Accession: 148319
A; Status: translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 1-379 < RES>
A; Cross-references: EMBL: X56790; NID:gi
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A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-379 < OAB>
A;Cross-references: GB:M32490; NID:g192909; PIDN:AAA37512.1; PID:g309206
A;Note: the authors translated the codon GAT for residue 337 as Gln
R;Latinkic, B.V.; O'Brien, T.P.; Lau, L.F.
Nucleic Acids Res. 19, 3261-3267, 1991
A;Title: Promoter function and structure of the growth factor-inducible immediate ear
A;Reference number: 148319; MUID:91288203; PMID:2062642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Gene: CYR61
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                                       KELGFDASEVELTRNNELIAVGKGRSLKRLPVFGMEPRILYNPL--QGQKCIVQTTSWSQ
                                                                                                                                                              MSSSTFRTLAVAVTLLHLTRLALSTCPAACHCPLEAPKCAPGVGLVRDGCGCCKVCAKQL
--LGLDASEVELTRNNELIAIGKGSSLKRLPVFGTEPRVLFNPLHAHGQKCIVQTTSWSQ
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A41428
CEF-10
R;Brunner, A.; Chinn, J.; Neubauer, M.; Purchio, A.F. DNA Cell Biol. 10, 293-300, 1991 A;Title: Identification of a gene family regulated by transforming A;Reference number: A40578; MUID:91229699; PMID:2029337
                                                beta IG-M2 protein precursor - mouse C;Speciaes: Mus musculus (house mouse) C;Date: 06-Mar-1992 #sequence_revision C;Accession: A40578; A53228 R;Brunner, A.; Chinn, J.; Neubauer, M.;
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A;Title: Identification of a phorbol ester-repressible v-src-inducible A;Reference number: A41428; MUID:89145206; PMID:2537491
A;Accession: A41428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Species: Gallus gallus (chicken)
C;Date: 03-Apr-1992 #sequence_revision 03-Apr-1992 #text_change
C;Accession: A41428
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A; Residues: 1-375 <SIM>
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                                                                                                                                                                                                                                                                          FTYAGCLSVKKYRFKYCGSCYDGRCCTPQLTRTVKMRFRCEDGETFSKNVMMIQSCKCNY
                                                                                                                                                                                                                                                                                                                         QCSKTCGTGISTRVTNDNPDCKLIKETRICEVRPCGQPSYASLKKGKKCTKTKKSPSPVR
                                                                                                                                                                                                                                                                                                                                         QCSKTCGTGISTRVTNDNPECRLVKETRICEVRPCGQPVYSSLKKGKKCSKTKKSPEPVR
                                                                                                                                                                                                                                                                                                                                                                                    SKEFGLDASEGELTRNNELIAIVKG-GLKMLPVFGSEPQSRAFENP----KCIVQTTSWS
                                                                                                                                                                                                                                                                                                                                                                                                     GKELGFDASEVELTRNNELIAVGKGRSLKRLPVFGMEP--RILYNPLQGQKCIVQTTSWS
                                                                                                                                                                                                                                                                                                                                                                                                                                                  QCTCIDGAVGCIPLCPQELSLPNLGCPSPRLVKVPGQCCEEWVCDES--KDALEELEGFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QCTCIDGAVGCIPLCPQELSLPNLGCPNPRLVKVTGQCCEEWVCDEDSIKDPMEDQDGLL 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LNEDCSRTQPCDHTKGLECNFGASPAATNGICRAQSEGRPCEYNSKIYQNGESFQPNCKH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LNEDCSKTQPCDHTKGLECNFGASSTALKGICRAQSEGRPCEYNSRIYQNGESFQPNCQH 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MSSRIARALALVYTLLHLTRLAL-STCPAACHCPLEAPKCAPGVGLVRDGCGCCKVCAKQ 59
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A; Residues: 1-349 < A; Cross-references:
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A;Description: Differential cloning and expression of human connective tissue gr
                                                                                                                                                                                                                                                                   A;Reference number: A40551; MUID:91373462; PMID:1654338 A;Accession: A40551
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A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-348 <BRUV
A;Cross-references: GB:M80263; NID:g201945; PIDN:AAA73135.1;
A;Cross-references: GB:M80263; NID:g201945; PIDN:AAA73135.1;
R;Ryseck, R.P.; Macdonald-Bravo, H.; Mattel, M.G.; Bravo, R.
Cell Growth Differ. 2, 225-233, 1991
Cell Growth Differ. 2, 225-233, 1991
                                                                                           A; Reference number: A; Accession: S44205
                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Homo sapiens (man)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change
                                           A; Molecule type:
                                                                A; Status: preliminary
                                                                                                                                                                                                                                  A; Molecule type: mRNA
A; Residues: 1-349 <BRA>
                                                                                                                                                                                                                                                                                                                                                R;Bradham, D.M.; Igarashi, A.; Potter, R.L.;
J. Cell Biol. 114, 1285-1294, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 connective tissue growth factor -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YNCPHANEAAFPFY--RLFNDI 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KFELSGCTSVKTYRAKFCGVCTDGRCCTPHRTTTLPVEFKCPDGEIMKKNMMFIKTCACH
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                     <OEM>
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Pred. No. 7.6
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                                                                                                                                                                                                                                                                                                                                                                        Grotendorst,
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EMBL: X78947; NID: g474933;

PID:g474934

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R;JOIlot, V.; Martinerie, C.; Dambrine, G.; Plassiart, G.; Brisac, M.; Crochet, J.;

MO1. Cell. Biol. 12, 10-21, 1992

A;Title: Proviral rearrangements and overexpression of a new cellular gene (nov) in A;Reference number: S20078; MUID:92107157; PMID:1309586

A;Accession: S20078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Gallus gallus (chicken)
C;Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jul-2000
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A; Residues: 1-351 < JOL>
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NOV protein -
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Best Local S
Matches 174
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Best Local
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                                                                                                                                                                            SKTQPCDHTKGLECNFGASSTALKGICRAQSEGRPCEYNSRIYQNGESFQPNCQHQCTCI
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                                                                                                                                                                                                                         LLLLLLLRPCEVSGREAACPRPCGGRCPAEPPRCAPGVPAVLDGCGCCLVCARQRGESC
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   SWSQCSKTCGTGISTRVTNDNPECRLVKETRICEVRPCGQPVYSSLKKGKKCSKTKKSPE
                                  AAYRQEATLGIDVSD-
                                                              ----KELGFDASEVELTRNNELIAVGKGRSLKRLPVFGMEPRILYNPLQGQKCIVQTT
                                                                                             DGQIGCLPRCNLGLLLPGPDCPFPRKIEVPGECCEKWVC-----DPRDEV--LLGGFAM
                                                                                                                                                          SPLLPCDESGGLYCDRGPEDGGGAGICMV-LEGDNCVFDGMIYRNGETFQPSCKYQCTCR
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46.6%; Pred. No. 1.9e-62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            348
                                                                                                                                                                                                                                                                                      ; Score 851.5; DB 2
; Pred. No. 2.1e-55;
44; Mismatches 104
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C; Species:
hypothetical protein Y47H9C.4 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 17-Mar-2000 C;Accession: T26972 R;Harris, B.
                                                                              RESULT 7
T26972
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C:Superfamily: thrombospondin type 1 repeat homology
F:203-250/Domain: thrombospondin type 1 repeat homology <THR1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Title: Structural analysis of the human nov proto-oncogene A;Reference number: I38069; MUID:94336229; PMID:7520150 A;Accession: I38069
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A; Residues: 1-357 < RES>
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C;Date: 17-May-1996 #sequence_revision 17-May-1996 #text_change
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                                                                                                                                                                                                        CCCCLTFLLLHLLGQVAATQRCPPQCPGRCPATPPTCAPGVRAVLDGCSCCLVCARQRGE
                                                                                                                                           NNEA 343
                                                                                                                                                                           ANEA 365
                                                                                                                                                                                                                          GCLSVKKYRPKYCGSCVDGRCCTPQLTRTVKMRFRCEDGETFSKNVMMIQSCKCNYNCPH
                                                                                                                                                                                                                                                                     CGMGFSTRVINRNRQCEMLKQTRLCMVRPCEQEPEQPTDKKGKKCLRTKKSLKAIHLQFK
                                                                                                                                                                                                                                                                                      CGTGISTRVINDNPECRLVKETRICEVRPCGQ-PVYSSLKKGKKCSKTKKSPEPVRFTYA 301
                                                                                                                                                                                                                                                                                                                                                                                                                   CIDGAVGCIPLCPQELSLPNLGCPNPRLVKVTGQCCEEWVCDEDSIKDPMEDQDGLLGKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SCSDLEPCDESSGLYCDRSADPSNQTGTCTA-VEGDNCVFDGVTYRSGEKFQPSCKFQCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RALALVVTLLHLTRLALST -- CPAAC -- HCPLEAPKCAPGVGLVRDGCGCCKVCAKQLNE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LAAYRPEATL---
                                                                                                                                                                                                                                                                                                                                                                                                  CRDGQIGCVPRCQLDVLLPEPNCPAPRKVEVPGECCEKWICGPD------EEDSLGGLT 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DCSKTQPCDHTKGLECNFGASSTALKGICRAQSEGRPCEYNSRIYQNGESFQPNCQHQCT 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CHGNCPQSNNAFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CNYNCPHANEAAF 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AVRFEYKNCTSVQTYKPRYCGLCNDGRCCTPHNTKTIQVEFRCPQGKFLKKPMMLINTCV 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PVRFTYAGCLSVKKYRPKYCGSCVDGRCCTPQLTRTVKMRFRCEDGETFSKNVMMIQSCK
                                                                                                                                                                                                                                                                                                                                                                 LGFDASEVELTRNNELIAVGKGRSLKRLPVFGMEPRILYNPLQGQKCIVQTTSWSQCSKT 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative, 48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL: X78351; NID: g587422; PIDN: CAA55146.1; PID: g825696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         39.1%; Score 827.5; DB 2; 43.1%; Pred. No. 1.2e-53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            339
                                                                                                                                                                                                                                                                                                                                     -----GVEVSD-----SSVNCIEQTTEWTACSKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches 120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Badzioch, M.; Saunders, G.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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39;

Gaps

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73 62

339

279

219

182 132 05-Nov-1999

expression

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Wilms Perb

Strong,

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A; Molecule type: DNA
A; Residues: 1-1620 <WIL>
A; Coss-references: EMBL:AL110498; NID:e1542303; PIDN:CAB54471.1; CESP:Y64G10A.
A; Experimental source: clone Y64G10A
C; Genetics:
                                                                                                                                                                                                                                                         hypothetical protein Y64G10A.f - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #tex C;Accession: T27283
                                                                                                                                                                                                                                                                                                                            RESULT
T27283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Experimental source: C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Status: F----
A; Molecule type: DNA
A; Residues: 1-1111 <WIL>
A; Cross-references: EMBL; AL032657; FA; Cross-references: Clone Y47H9C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       submitted to the EMBL Data Library A; Reference number: Z20293 A; Accession: T26972 A; Status: preliminary; translated
                                                                                                                                                                                                          R;Ainscough, R. submitted to the EMBL Data Library, A;Reference number: Z20336
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A;Introns: 50/2; 84/2; 150/1; 238/3; 342/3; 797/1; C;Superfamily: unassigned ankyrin repeat proteins;
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                                                                Gene: CESP:Y64G10A.f
Introns: 77/1; 116/1;
                                Query Match
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Best Local (
 Matches
                Local
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 92;
                  Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                          NCPHAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VKKYRPKYCGSCVDGRCCTPQLTRTV-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNPECRLVKETRICEVRPCGQPVYSSLKKGKKCSKTKKSPEPVRFTY-----AGCLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RNNELIAVGKGRSLKRLPVFGMEPRILYNPLQGQKCIVQTTSWSQCSKTCGTGISTRVTN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CDRGWTGHRCEHHCPADTFGANCEKRCKCPKGIGCDPITGECTCPAGLQGANCDIGCPEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NPETGSC----VCKPGRTGKNCSEPCPL----DFYGPNCAHQCQCNQRGVGCDGADGKCQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NFGASSTALKGICRAQSEGRPCEYNSRIYQNGESFQPNCQHQCTC-----IDGA----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CSKTCTCVRENTLMCAPNTGFCRCKPGFYGDNCELACSKDSYGPNCEKQAMCDWNHASEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CPAACHCPLE-APKCAPGVGLVR-----DGCGCCKVCAK-QLNEDCSKTQPCDHTKGLEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CDQKCDPNTFGFLCQETVTPSPCASTDPKNGVCLSCPPGSSGIHCEHNCPAGSYGDGCQQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SYGPGCKLHCKCVNGKCDKETGEC----TC-----
   Conservative
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                                                              198/1; 282/1; 365/1; 425/1; 466/1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          -SCADGHGCDPTTGECICEPGYHGKTCSEKCPDGKYGYGCALDCPKCASGS
               8.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8.2%; Score 174; DB 2;
19.7%; Pred. No. 4.3e-05;
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 Pred. No. 6.8e-05;
3; Mismatches 146
                                Score 173.5;
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                                                                                                                                                                                                                            September
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                                                                                                                                                                                                                                1999
                                DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -KMRFRCEDGETFSKNVMMIQSCKCNY
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   146;
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                                                                                                                                                                                                                                                                           #text_change
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                              Length 1620;
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 Indels
                                                              548/1;
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 109;
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                                                                 559/1;
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                                                                601/1;
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J. MOl. Biol. 211, 331-349, 1990
A;Title: The balbiani ring 3 gene in Chironomus tentans
A;Reference number: S08167; MUID:90172404; PMID:1889777
A;Accession: S08167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Balbiani ring 3 protein - midge (Chiron C; Species: Chironomus tentans C; Date: 30-Sep-1991 #sequence_revision C; Accession: S08167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT
S08167
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C; Superfamily: unassigned
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A; Residues: 1-17
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                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                            CICPTAEPAGGCSAPLKWDDDKCSCACPAKMEEKKEKCVESGKIWNPNTCECGCAQLNCP
                                                                                                                                                                                                                                                                                         CHCPLEAPK - - CAPGVGLVRDGCGC - CKVCAKQLNEDCSKTQPCDHTKGLEC - - - - NFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LGFDASEVELTRNNELIAVGKGRSLKRLPVFGMEPRILYNPLQGQKCIVQT-----TSW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CSNGA----SCDRVTGF--CDCPSGFMGKNCESECPEGLWGSNCMKHCLCMHGGECNKE 1206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CIDGAVGCIPLCPQELSLPNLGCPNPRLVKVTGQCCEEWVCDEDSIKDPMEDQDGLLGKE 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YNPFVARCDHVTG-ECR----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CKGICSCQNGATCDSVTGSCECRPGWRGKKCDRPCPDG--RFGEGCNAICDCTTTNDTSM 1109
 QMSPGGCGSGKSFNKLTCQCECDQSASKCGLKRWNADTCKCECQPGMPPEGCGKQTWISD
                                                                                                                                                            DGAYGCIPLCPQELSLPNLGCPNPRLVKVTGQCCEEWVCDEDSIKDPMEDQDGLLGKELG
                                                                                                                                                                                            DNKKANKETCQCECKEVKKC-----NGGQVF---CKDSCSCVCPGGDKDKTCTAPQVY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              S--QCSKTCGTGISTRVTNDNPECRLVKETRICEVRPCGQPVYSSLK-----KGKKCSKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CPAACHCPLEAP----
                                SQCSKTCGTGISTRVTNDNPEC - - -
                                                                ETICQCICPRDAPVCTAGKERCGESCECKCINREPKEGCAKPLVWNE-NTCKCVCPADK-
                                                                                              FDASEVELTRNNELIAVGKGR-----
                                                                                                                                DG-VACSCSCPVNMQKPADGCPRP
                                                                                                                                                                                                                            ASSTALKGICRAQ-SEGRPCEYNSRIYQNGESFQPNCQHQCTCI---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DG-TFGESCS--QKCDCGEN 1369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DGETFSKNVMMIQSCKCNYN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KKSPEPVRFTYAGCLSVKKYRPKYCG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SGEHCEKSCVSG-----HYGAKC---EETCECENGALCDPISGHCSCQPGWRGKKCNRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NG-----DCECIDGWTGPSLCPFGQFGRNCAQRCNCKNGASCDRKTGRCECLPGW
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                                                                                                                                                                                                                                                                                                                          Conservative
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GB:X52263;
                                                                                                                                                                                                                                                                                                                                          7.48; 20.98;
                                                                                                                                                                                                                                                                                                                                                                                         Balbiani ring
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                                                                                                                                                                                                                                                                                                                            47;
                                                                                                                                                                                                                                                                                                                                        Score 157;
Pred. No. 0.
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                                                                                                -SLKRLPVFGMEPRILYNPLQGQKCIVQTTSW
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.0012;
                                   RLVKETRICEVRP-----CGQPVYSSL
                                                                                                                                 -QKWDKEECRCECPVK-HDCKNGKVWD
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A; Title: Identification of high-molecular-weight prote
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         80
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zonadhesin -
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A;Experimental source: strain Sprague-Dawley; brain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: mRNA
A; Residues: 1-1574 <NAK>
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Best Local :
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97; Conserv
mouse
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                                                                                                             NVMMIQSCKCNYN -- CPHANEA
                                                                                                                                                                           AGCLSVKKYRPKYC----GSC--VDGRC-CT-----PQLTRTVKMRF----RCEDGETFSK 345
                                                                                                                                                                                                                                                                                                                                                                                                      AGFQGERCQAEC---ESG-FFGPGCRHRCTCQPG-VACDPVSGECRTQCPPGYQGEDCGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                      AQSEGRPCEYNSRIYQNGESFQPNCQHQCTCIDGAVGCIPL------
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Pred. No. 0.0021
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R;Lawler, J.; Duquette, M.; retroy...
J. Biol. Chem. 266, 8039-8043, 1991
A;Title: Cloning and sequencing of chicken
A;Reference number: A39804; MUID:91217026;
A;Accession: A39804
A;Status: preliminary
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                       RESULT 12
A39804
A;Molecule type: mRNĀ
A;Residues: 1-1178 <LAW>
A;Residues: 1-1178 <LAW>
A;Cross-references: GB:M60853; NID:g212763; PIDN:AAA51437.1; PID:g212764
A;Cross-references: GB:M60853; NID:g212763; PIDN:AAA51437.1; PID:g212764
C;Superfamily: thrombospondin 1; EGF homology; thrombospondin type 1 repeat homology <VWC>
F;325-383/Domain: thrombospondin type 1 repeat homology <THR1>
F;386-437/Domain: thrombospondin type 1 repeat homology <THR2>
                                                                                                                                                                                                                                                                                        thrombospondin precursor - chicken
C;Species: Gallus gallus (chicken)
C;Date: 10-Sep-1999 #sequence_revision
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Description: functions
A; Note: found exclusively
C; Keywords: cell adhesion
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C; Function:
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A; Residues: 1-5376 <G;
A; Cross-references: El
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J. Biol. Chem. 273,
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TRLALSTCPAACHCPLEAPKCAPGVGLVRDGCGCCKVCAKQLNEDCSKTQPCDHTKGLEC 78
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Pred. No. 0.00
39; Mismatches
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C:Species: Rattus norvegicus (Norway rat)
C:Date: 04-Mar-1993 #sequence_revision 18
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A;Title: cDNA for the carboxyl-terminal region of a rat A;Reference number: A42112; MUID:92184794; PMID:1371999
A;Accession: A42112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Experimental source: intestine
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F;658-697/Domain:
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Best Local :
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                                     HCIIKRPEQQYIILKPGEIQKNPNDRCTFFSCMKI--
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EPRILYNPLQGQKCIVQTTSW--SQCSKTCGTGISTRVTNDNPECRLVKETRICEVRPCG
                                                                                                                                                                               TTSCKCDPKRCKAERPSCLLGFEVKSEHVPGKCCPVYSCVPKGVCVHENAEYQPGSPVYS
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                                                                                                         NKCQDCVCTDSMDNSTQLNVISCTHVP-C----NISCSSGFELVEVPGECCKKCQQT
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23.0%;
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                                                                                                                                           -GAVGC--IPLCPQELSLPNLGCPNP-RLVKVTGQCCEEWVCD
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                                                                                                                                                                                                                                                                                                                                                                                                                        Score 150; DB 2;
Pred. No. 0.0019;
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                                                                                                                                                                                                                    -FGASSTALKGICRAQSEGRP---CEYNSRIYQNGESFQP
                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches 138;
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                                                                     - FDASEVELTRNNELIAVGKGRSLKRLPVFGM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  laminin Blk chain precursor - human N;Alternate names: kalinin Bl chain; nicein Bl
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A; Residues: 1-1170 <GER>
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A; Title: The complete
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Best Local
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Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 05-Nov-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             249
                                                                                                                                                                                                                                                    224 LQGQKCIVQTTSWSQCSKTCGTGISTRVTNDNP-----ECRLV------KETRICEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   774
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     274 Q-PVYSSLKKGKKCSKTKKSPEPVRFTYAGCLSVKKYRPKYC-GSC--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         64 CSKTQPCDHTKGLECN-----FGASSTALKGI---CRAQSEGRPCE----YNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29 ACHCPLEAPKCAPGVGL------VRDGCGC------CKVCAKQLN------ED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                     GFGGLMCSAAAIR-----
                                                                                                                                         LPNVVGPKCDQCAPYHWKLASGQGCEPCACDPHN----
                                                                                                                                                                           RP-----CGQ--PVYSSLKKGKKCSKTKKSPEPVRFTYAGCLSVKKYRPKYCGSC----
                                                                                                                                                                                                                    VQGERC
                                                                                                                                                                                                                                                                                                                            DEDSIKDPMEDQDGLLGKELGFDASEVELTRNNELIAVGKGRSLKRLPVFGMEPRILYNP
                                                                                                                                                                                                                                                                                                                                                                                                  RIYONGESFOPNCOHOCTC-IDGAVGCIPLCPOELSLPNLGCPNPRLVKVTGOCCEEWVC
                                                                                                                                                                                                                                                                                                                                                                                                                                     AHECQRCD-----CNGHSETCHFDPAVFAASQGAYGGVCDNCRDHTEGKNCERCQLHYF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SCFCHGHADRCAPKPGASAGSTAVQVHDVCVCQHNTAGPNCERCAPFYNNRPWRPAEGQD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HGCSCCREERTSVRMVSLDCPDGSKLSHSYTHIESCLC
                                                                                                                                                                                                                                                                                                                                                                  RNRRPGASIQETC - ISCECDPDGAVAGAPCDP - - -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 G--RCCTPQLTRTVKMRFRCEDGETFSKNVMMIQSCKC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               명 <del>'</del>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wagman, D.W.; Champliaud, M.F.; Burgeson, 59, 11073-11080, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -SDCVPGSITYMPNGCCKTC-----IHNPN---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7.0%;
                                                                                                                                                                                                                 -DLCKPGF-TGLTYANPRRCHRCDCNILGSREMPCDEESGRCLC
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                                                                     -QCPD-RTYGDVATGCRACDCDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 147.5;
Pred. No. 0.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .0041;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 2;
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                                                                                                                                           SLSPQCNQFTGQCPCRE
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R;Map Position: 17
A;Introns: 22/1; 49/2; 148/1; 264/1; 305/1; 384/1; 436/1; 501/1; 539/1; 577/1; 618/1; 67
A;Introns: 22/1; 49/2; 1761/3
1679/3; 1729/1; 1761/3
C;Superfamily: notch protein; ankyrin repeat homology; EGF homology
C;Superfamily: notch protein; ankyrin repeat homology; EGF homology
C;Superfamily: notch protein; ankyrin repeat homology; EGF homology
C;Superfamily: notch protein; ankyrin repeat homology; EGF homology
C;Superfamily: notch protein; ankyrin repeat homology; EGF homology
C;Superfamily: notch protein; ankyrin repeat homology; EGF homology
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                                                                                                                                                                                      QΥ
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Best Local S
Matches 94
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Molecule type: DNA
Residues: 1-1964 <ROW>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 690 GGCIST-PCAHGGTCHPOPS-----GYNCTCPAGYMGLTCSEEVTACHSGPC-----
                                                                                                                                                                                                                                                                                                                                                                                                                   634 GQ----QCQGQEHRAPCLCPDGSPGCVPAEDNCPCHHGHCQRSLCVCDEGWTGPECETEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                               110 GESFQPNCQHQ-----CTCIDGAVGCIPL------CPQELSLPNLGCPNPRLVKVT 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           574 CLPGFEGPHCEKEVDECLSDPCPVGASCLDLPGAFFCLCRPGFTGQLCEVPLCTPNMCQP 633
                                                                                                                                                                                                                                                                                                                                                                     155 GQCCEEWVCDEDSIKDPMEDQDGLLGKELGFDASEVELTRNNELIAVGKGRSLKRLPVFG 214
                                                                                                                                                                                                                                           736
                                                                                                                                                                                                                                                                                  215 MEPRILYNPLOGOKCIVQTTSWSQCSKTCGTGISTRVTNDNPECRLVKETRICE--VRPC 272
                                                                                                                                                                                             273 GQPVYSSLKKGKKCSKTKKSÞEPVRFTYAGCLSVKKYRPKYC-----GSCVDGRC----- 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28 AACHCPLEAPK--CAPGVGLVRDGCGCCKVCAKQLNEDCSKT------QP----QD 71
                                                                                                     323 C--TPQLTRTVKMRFRCEDGETFSKNVMMIQSCKCNYNCPH 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       72 HTKGLE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                   ---VSASCLNGGTCVN----KPGTFF---CLCATGFQGLHCEEKTNPSCADSPCRNKAT 817
                                                            CQDTPRGARCL----CSPGYTGSSCQTLIDLC-ARKPCPH 852
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6.9%; Score 146; DB 2; L
ilarity 23.4%; Pred. No. 0.0086;
Conservative 28; Mismatches 141;
                                                                                                                                                                                                                                             -LNGGSCSIRPEGYSCTCLPSHTG--
5, 2003, 14:07:29
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Search completed: August Job time : 17.5408 secs

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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence:
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             Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Gapop 10.0 , Gapext 0.5
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2116
1 MSSRIARALALVVTLLHLTR.....ANEAAFPFYRLFNDIHKFRD
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        DB
  CYR6_HUMAN
CYR6_RAT
CYR6_RAT
CE10_CHICK
CTGF_ROT
CTGF_MOUSE
CTGF_HUMAN
CTGF_PIG
NOV_COTJA
NOV_HUMAN
NOV_XENLA
NOV_HUMAN
NOV_XENLA
NOV_HUMAN
NOV_KENLA
NOV_HOUSE
NOV_RAT
BARJ_CHICK
TMAL_HUMAN
ZAN_MOUSE
TMAL_HUMAN
ZAN_MOUSE
TMAL_HUMAN
TSP1_CHICK
NTC4_MOUSE
TMS2_CHICK
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000622 homo sapien P18406 mus musculu Ques72 rattus norv P19336 gallus gall garley ratus sorv P1936 mus musculu P29268 mus musculu P29279 homo sapien O1873 bos taurus O19113 sus scrofa P28686 gallus gall P42642 coturnix co P48745 homo sapien P51609 kenopus lae 064299 mus musculu 092765 rattus norv O76076 homo sapien 09204 mus musculu 091766 rattus norv O18376 chironomus P57999 oryctolagus P244043 homo sapien O18799 mus musculu P35440 gallus gall P98089 rattus norv O1675 mus musculu P35440 gallus gall P31695 mus musculu P35440 gallus gall P31695 mus musculu P35448 mus musculu 013751 homo sapien O1817 homo sapien O1817 homo sapien O1817 homo sapien O1817 homo sapien O18178 bos taurus C18178
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	45	44	43	42	4.1	40	39	38	37	36	35	34
	135	135	135	136.5	137	137	137	137.5	138.5	139	139	139
	6.4	6.4	6.4	6.5	6.5	6.5	6.5	6.5	6.5	6.6	6.6	6.6
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•	Q28295 canis famil	P35441 mus musculu	Q61087 mus musculu	P59222 mus musculu	Q07008 rattus norv	Q96gp6 homo sapien	P83110 homo sapien	P24014 drosophila	P07207 drosophila	Q28833 sus scrofa	P46530 brachydanio	Q9y6n6 homo sapien

ALIGNMENTS

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to the EMBL/GenBank/DDBJ databases. ble M., Liu J., Chow C., Sadowski I.; ression of the CYR61 gene in normal human to the EMBL/GenBank/DDBJ databases.	SEQUENCE FROM N.A. SEQUENCE FROM N.A. TISSUE-placenta; Kolesnikova T.V., Lau L.F.; Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases. SEQUENCE FROM N.A. Bi A.B., Yu L.; Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases. [6] SEQUENCE FROM N.A. Schuetze ROM N.A. Schuetze N., Lechner A., Groll C., Koehrle J., Jakob F.; "Regulation of hCYR61 by vitamin D, serum and cytokines in fetal human	SEQUENCE FROM N.A. SEQUENCE FROM N.A. MEDLINE-97280750; PubMed-9135077; Jay P., Berge-Lefranc J.L., Marsollier C., Mejean C., Taviaux S., Berta P.; "The human growth factor-inducible immediate early gene, CYR61, maps to chromosome 1p."; Oncogene 14:1753-1757(1997). [3] SEQUENCE FROM N.A. MEDLINE-98197344; PubMed-9536281; MARTINETIE C., Viegas-Pequignot E., Nguyen V.C., Perbal B.; "Chromosomal mapping and expression of the human cyr61 gene in tumour cells from the nervous system."; Mol. Pathol. 50:310-316(1997). [4]	

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RX MEDLINE=22388557; pubMed=12477932;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Schaefer C.F., Bhat N.K.,

RA Alteschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

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RA HOpkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hong L.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

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RA Brownstein M.J., Wedlan D. R., Feters G.J., Abramson R.D., Mullahy S.J.,

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RA Brownstein S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulk S.W.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulk S.W.,

RA Willalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

RA Wilting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Wilting M., Tuchman J.W., Green E.D., Dickson M.C.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

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RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.
Pfam; PF00007; Cys_knot; 1
Pfam; PF00009; tsp_1; 1.
Pfam; PF00090; tsp_1; 1.
Pfam; PF00090; vwc; 1
SMART; SM00041; CT; 1.
SMART; SM00121; IB; 1.
SMART; SM0020; TSP1; 1.
SMART; SM00204; CTCK_1;
PROSITE; PS01185; CTCK_2;
PROSITE; PS01225; CTCK_2;
PROSITE; PS01225; TGF_BND
PROSITE; PS00222; TGF_BND
PROSITE; PS01092; TSP1; 1.
PROSITE; PS01092; TSP1; 1.
PROSITE; PS01093; TSP1; 1.
PROSITE; PS01094; VWFC_1;
PROSITE; PS01040; VWFC_2;
PROSITE; PS01040; VWFC_2;
PROSITE; PS01040; VWFC_3;
PROSITE; PS01040; VWFC_3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
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SUBCELULIAR LOCATION: Secreted.
SIMILARITY: Contains 1 IGFBP domain.
SIMILARITY: Contains 1 VWFC domain.
SIMILARITY: Contains 1 TSP type-1 domain.
SIMILARITY: Contains 1 C-terminal cystine knot-like (CTCK)
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IPR000867; Insl_gro_fac_pr.
IPR000884; TSP1.
IPR001007; VWF_C.
                                  CTCK_1; 1.
CTCK_2; 1.
IGF_BINDING;
ITSP1; 1.
VWFC_1; 1.
VWFC_2; 1.
           Signal
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STRAIN-BALB/c; TISSUE-Fibroblast;
MEDLINE-90287146; PubMed-2355916;
MEDLINE-90287146; PubMed-2355916;
O'Brien T.P., Yang G.P., Sanders L., Lau L.F.;
O'Brien T.P., Yang G.P., Sanders L., Lau L.F.;
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01-NOV-1990 (Rel. 16, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
CYR61 protein precursor (Cysteine-rich, angiogenic inducer,
(Insulin-lke growth factor-binding protein 10) (3CH61).
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Best Local
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Pfam; PF00219; IGFBP; 1
Pfam; PF00090; tsp_1; 1
Pfam; PF00093; vwc; 1.
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SMART;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FF
STRAIN-AJ;
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InterPro; IPR006207; Cys_knot_C.
InterPro; IPR0008667; Insl_gro_fac_pr.
InterPro; IPR000884, Tspl.
InterPro; IPR001007; VWF_C.
Pfam; PF00007; Cys_knot; 1.
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EMBL; X56790; CAA40109.1;
PIR; A35669; A35669.
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Latinkic B.V., O'Brien T.P., Lau L.F.;
"Promoter function and structure of the growth f
immediate early gene cyr61.";
Nucleic Acids Res. 19:3261-3267(1991).
"In COLUMN ANY ACT AS ONE OF THE MANY GROWTH
PROTEINS; PROMOTES PROLIFERATION, MIGRATION
TO SUBCOTITUDE TO CONTINUE.
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MEDLINE-91288203; PubMed-200
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                                                                                                                     Match
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SIMILARITY: Contains 1 IGFBP domain.
SIMILARITY: Contains 1 VWFC domain.
SIMILARITY: Contains 1 TSP type-1 domain.
SIMILARITY: Contains 1 TSP type-1 domain.
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TISSUE SPECIFICITY: LOW IN KIDNEY,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AND OVARY, MODERATE IN HEART,
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SM00121; IB; 1.
SM00209; TSP1; 1
SM00214; VWC; 1.
                                                                                               Similarity
PS00222;
PS50092;
                                                                                                                                                                                                                                                                                                                                                                                                                                             PS01185; CTCK_1; 1.
PS01225; CTCK_2; 1.
PS00222; IGF_BINDING;
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;; VWFC_1; 1.
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                                                                   Score 1929; pred. No. 6.5e. 10; Mismatches
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No. 6.5e-133;
smatches 19;
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28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
CYR61 protein precursor (Cysteine-rich, angiogenic inducer,
(Insulin-like growth factor-binding protein 10).
CYR61 OR IGFBp10.
                                                                                                                                                                                                -!- SUBCELLULĀR I
-!- SIMILARITY: (
-!- SIMILARITY: (
-!- SIMILARITY: (
         InterPro;
InterPro;
InterPro;
                                           InterPro;
InterPro;
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Q9ES72;
                                                                                         use by non-profit institutions as long a
modified and this statement is not removed:
entities requires a license agreement (See
or send an email to license@isb-sib.ch).
                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                  Albrecht C., von Der Kammer Nitsch R.M.;
                                                                                                                                                                                                                                                                                                                                                                                     Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM
                                                                    EMBL; AF218568; AAG14964.1;
                                                                                                                                                                                                                                                       "Muscarinic acetylcholine receptors induce the e
immediate early growth regulatory gene CYR61.";
J. Biol. Chem. 275:28929-28936(2000).
-1- FUNCTION: MAY ACT AS ONE OF THE MANY GROWTH
PROTEINS; PROMOTES PROLIFERATION, MIGRATION
                                                                                                                                                                                                                                                                                                                                          MEDLINE-20435857;
                                                                                                                                                                                                                                                                                                                                                      TISSUE-Lung
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SIMILARITY: Contains 1 VWFC domain.
SIMILARITY: Contains 1 TSP type-1 domain.
SIMILARITY: Contains 1 C-terminal cystine knot-like (CTCK) domain.
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                               IPR006208; Cys_knot.
IPR006207; Cys_knot_C.
IPR000867; Insl_gro_fac_pr.
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AND ADHESION ()
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IPR000884; IPR001007;

TSP1

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RESULT 4
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ID CELO_C
AC P19336
DT 01-NOV
DT 15-SEP
DE CEF-10
OS Gallus
OC Eukary
OC Archos
OC Gallus
OX NCBI_T
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Best Local Sin
Matches 348;
                                     01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
15-SEP-203 (Rel. 42, Last annotation update)
CEF-10 protein precursor.
Gallus gallus (Chiorea)
                                                                                    CE10_CHICK
P19336;
01-NOV-1990
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SEQUENCE
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                                CEF-10 protein precursor. Gallus gallus (Chicken). Eukaryota; Metazoa; Chord
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  NCBI_TaxID=9031;
            Archosauria; Aves; Gallus.
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; PF00093; vwc; 1.
r; SM00041; CT; 1.
r; SM00121; IB; 1.
r; SM00209; TSP1; 1.
r; SM00204; VWC; 1.
iTE; PS01185; CTCK_1
iTE; PS01125; CTCK_2
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;; PS00222; IGF_BINDING; 1
3; PS50092; TSP1; 1.
3; PS01208; VWFC_1; 1.
E: PS50184; VWFC_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                               1 MSSRIARALALVVTLLHLTRLALSTCPAACHCPLEAPKCAPGVGLVRDGCGCCKVCAKQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity 90.9
18; Conservative
                                                                                                                                                                        CPHANEAAFPFYRLFNDIHKFRD
                                                                                                                                                                                                                TYAGCLSVKKYRPKYCGSCVDGRCCTPQLTRTVKMRFRCEDGETFSKNVMMIQSCKCNYN
                                                                                                                                                                                                                                                            CSKTCGTGISTRVTNDNPECRLVKETRICEVRPCGQPVYSSLKKGKKCSKTKKSPEPVRF
                                                                                                                                                                                                                                                                                                                                               CTCIDGAVGCIPLCPQELSLPNLGCPNPRLVKYTGQCCEEWVCDEDSIKDPMEDQDG1LG
                                                                                                                                                                                                                                                                                                                                                                            NEDCSKTQPCDHTKGLECNFGASSTALKGICRAQSEGRPCEYNSRIYQNGESFQPNCQHQ.
                                                                                                                                                             CPHPNEASFRLYSLFNDIHKFRD
                                                                                                                                                                                                     TYAGCSSVKKYRPKYCGSCVDGRCCTPLQTRTVKMRFRCEDGEMFSKNVMMIQSCKCNYN
                                                                                                                                                                                                                                                CSKSCGTGISTRVTNDNSECRLVKETRICEVRPCGQPVYSSLKKGKKCSKTKKSPEPVRF
                                                                                                                                                                                                                                                                                         --LGFDASEVELTRNNELIAIGKGSSLKRLPVFGTEPRVLYNPLHAHGQKCIVQTTSWSQ
                                                                                                                                                                                                                                                                                                     KELGFDASEYELTRNNELIAVGKGRSLKRLPVFGMEPRILYNPL--QGQKCIVQTTSWSQ
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41687 MW;
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                      Neognathae;
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90.9%;
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Pred. No. 6.5e-133;
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                      Craniata; Vertebrata; Euteleostomi;
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Pfam; PF00090; tsp_1;
Pfam; PF00093; vwc; 1.
SMART; SM00041; CT; 1.
SMART; SM00121; IB; 1.
SMART; SM00121; VWC; 1.
SMART; SM00214; VWC; 1.
PROSITE; PS01185; CTCK,
PROSITE; PS01125; CTCK,
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-!- SIMILARITY: Contains 1 VI-

-!- SIMILARITY: Contains 1 T.
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InterPro; IPR006207; Cys_knot_C.
InterPro; IPR000867; Insl_gro_fac_pr.
InterPro; IPR000884; Tspl.
InterPro; IPR0010884; Tspl.
InterPro; IPR001007; VWF_C.
Pfam; PF00007; Cys_knot; 1.
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PIR; A41428; A41428
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Proc. Natl. Acad. Sci. U.S. A. 86:1178-1182(1989).
-!- FUNCTION: PROBABLE SECRETED REGULATORY PROTEIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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3; PS01225; CTCK_2; 1.
3; PS00222; IGP_BINDING; 1
6; PS50092; TSP1; 1.
6; PS01208; VWFC_1; 1.
6; PS50184; VWFC_2; 1.
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VWFC domain.

TSP type-1 domain.

C-terminal cystine knot-like (CTCK) domain.
                                                                                                                                                                                                                                                                               20;
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Pred. No. 5.8e
Pred. Mismatches
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VWFC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

MEDLINE=20145935; PubMed=10679821;

MU J., Smock S.L., Safadi F.F., Rosenzweig A.B., (

Marks S.C. Jr., Owen T.A., Popoff S.N.;

"Cloning the full-length cDNA for rat connective implications for skeletal development.";

"-11. Biochem. 77:103-115(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Rattus norvegicus connective tissue growth factor.";
Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: MAJOR CONNECTIVE TISSUE MITOAGTTRACTART SECRETED BY
VASCULAR ENDOTHELIAL CELLS. PROMOTES PROLIFERATION AND
DIFFERENTIATION OF CHONDROCYTES (BY SIMILARITY). MEDIATES CELL
ADHESION AND ENHANCES FIRROBLAST GROWTH FACTOR-INDUCED DNA
SYNTHESIS (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: Contains 1 IGFBP domain.
-!- SIMILARITY: Contains 1 TSP type-1 domain.
-!- SIMILARITY: Contains 1 TSP type-1 domain.
-!- SIMILARITY: Contains 1 TSP type-1 domain.
                           Pfam;
Pfam;
Pfam;
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                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                  Pfam;
                                                                                                                                                                                                   Interpro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                            InterPro;
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                                                                                                                                                                         InterPro;
                                                                                                                                                                                                                          InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CTGF_RAT
                                                PF00219;
                                                                                                                                                                                                                                           AF120275; AAD39132.1; -.
                                                                                           Pro: IPR006208; Cys_knot.
Pro: IPR006207; Cys_knot_C.
Pro: IPR000867; Insl_gro_fac_pr.
Pro: IPR000884; TSpl.
Pro: IPR001007; VWF_C.
PR00007; Cys_knot; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      358
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                         ; IGFBP; 1.
; tsp_1; 1.
; vwc; 1.
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CTGF_MOUSE
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SMART; SM00214; VWC; 1.

PROSITE; PS01185; CTCK_1; 1.

PROSITE; PS01225; CTCK_2; 1.

PROSITE; PS00222; IGF_BINDING; 1

PROSITE; PS00092; TSP1; 1.

PROSITE; PS01208; VWFC_1; 1.

PROSITE; PS01208; VWFC_2; 1.
                                                                                                                                                                                                                                         CTGF_MOUSE
P29268; Q922U0;
01-DEC-1992 (Re
                                                                                                               01-DEC-1992 (Rel. 24, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation updat
Connective tissue growth factor precursor (
(Hypertrophic chondrocyte-specific protein
CTGF OR FISP12 OR FISP-12 OR HCS24.
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                 Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=10090;
                                                                                           Mus musculus (Mouse)
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347
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37756 MW;
                                             Rodentia;
                                                                       Chordata;
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46.2%;
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Pred. No. 2.2e-
58; Mismatches
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CTCK.
BY SIMILARITY.
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A -> P (IN REF.
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                                             Sciurognathi; Muridae;
                                                                       Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CONNECTIVE TISSUE
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                                                                                                                                                                                                                                                                                            348
                                                                                                                                                                                           update)
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                                             Murinae;
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RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Bitchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Robak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Wilting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Godriguez A.C., Shevchanko Y., Marra M.A.;
Ra Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Babic A.M., Chen C.C., Lau L.F.;

"Fisp12/mouse connective tissue growth factor mediates endothelial cell adhesion and migration through integrin alphavbeta3, promotes endothelial cell survival, and induces angiogenesis in vivo.";

MOI. Cell. Biol. 19:2958-2966(1999).

-!- FUNCTION: MAJOR CONNECTIVE TISSUE MITOATTRACTANT SECRETED BY VASCULAR ENDOTHELIAL CELLS. PROMOTES PROLIFERATION AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Brunner A., Chinn J., "Identification of a factor-beta.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kireeva M.L., Latinkic B.V., KOLEBILACVIL ...,
Abler A.S., Lau L.F.;
*Cyr61 and Fisp12 are both ECM-associated signaling molecules:
*Cyr61 and Fisp12 are both ECM-associated signaling molecules:
                                                                                                                                                                This
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Exp. Cell Res. 233:63-77(1997).
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"Structure, mapping, and expression of fisp-12, a
inducible gene encoding a secreted cysteine-rich
Cell Growth Differ. 2:225-233(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DIFFERENTIATION OF CHONDROCYTES (BY SIMILA ADDRESSION AND ENHANCES FIBROBLAST GROWTH FA SYNTHESIS (BY SIMILARITY).

SUBUNIT: MONOMER (BY SIMILARITY).

SUBCELLULAR LOCATION: FOUND IN THE EXTRACE SOLUBLE FORM.

TISSUE SPECIFICITY: TESTIS, SPLEEN, KIDNEY (LOMEST LEVEL IN TESTIS AND HIGHEST IN LUN TESTIS AND HIGHEST HIGHEST HIGHEST HIGHEST HIGHEST HIGHEST HIGHEST HIGHEST HIGHEST HIGHEST HIGHEST HIGHEST HIGHEST HIGHEST HIGHEST HIGHEST HIGHEST HIGHEST HIGHEST HIGHEST HIGHEST HIGHEST HIGHEST HIGHEST HIGHEST HIGHEST HIGHEST HIGHEST HIGHEST HIGHEST HIGHEST HIGHEST HIGHEST HIGHEST HIGHEST HIGHEST HIGHEST HIGHEST HIGHEST HIGHEST HIGHEST HIGHEST HIGHEST HIGHEST HIGHEST HIGHEST HIGHEST HIGHEST HIGHEST HIGHEST HIGHEST HIGHEST HIGHEST HIGHEST HIGHEST HIGHEST HIGHEST HIGHEST HIGHEST HIGHEST HIGHEST HIGHEST HIGHEST HIGHEST HIGHEST HIGHEST HIGHEST HIGHEST 
                                                                                                                                                                                                                SIMILARITY: Contains 1 IGFBP domain.
SIMILARITY: Contains 1 VWFC domain.
SIMILARITY: Contains 1 TSP type-1 domain.
SIMILARITY: Contains 1 C-terminal cystine knot-like (CTCK)
                                                ween the Swiss Institute of Bioinformatics Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INDUCTION: By growth
                                                                                                     SWISS-PROT entry is copyright. It is produced through a collaboration sen the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Biol.
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There are no restrictions ong as its content is in
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Best Local
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Pfam; PF00093; vwc; 1.
Pfam; PF00093; vwc; 1.
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InterPro; IPR006207; Cys_knot_C.
InterPro; IPR000867; Insl_gro_fac_pr.
InterPro; IPR000884; TSp1.
InterPro; IPR001007; VWF_C.
Pfam; PF00007; Cys_knot; 1.
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GC); GC:0005578; C:extracellular matrix; IDA.

GC; GC:0008201; F:haparin binding activity; II

GC; GC:0005178; F:integrin binding activity; II

GC; GC:0001525; P:angiogenesis; IDA.

GC; GC:00016477; P:cell matrix adhesion; IDA.

GC; GC:0007160; P:cell-matrix adhesion; IDA.

GC; GC:0008543; P:FGF receptor signaling path
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PF00219; IGFBP; 1.
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PS50092;
PS01208;
SQCSKTCGTGISTRVTNDNPECRLVKETRICEVRPCGQPVYSSLKKGKKCSKTKKSPEPV
                                                                                                                             QHQCTCIDGAVGCIPLCPQELSLPNLGCPNPRLVKVTGQCCEEWVCDEDSIKDPMEDQDG::||||:|||||||||
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                                                         KQLGELCTERDPCDPHKGLFCDFGSPANRKIGVCTAK-DGAPCVFGGSVYRSGESFQSSC
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AAA73135.1; -.
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46.6%;
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RESULT
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                                                     Nakanishi T., Nishida T., Shimo T., Kobayashi K., Kubo Tamatani T., Tezuka K., Takigawa M.;
"Effects of CTGF/Hcs24, a product of a hypertrophic chorspecific gene, on the proliferation and differentiation chondrocytes in culture.";
                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE-Umbilical vein endothelial cell MEDLINE-93187114; PubMed-1293144; Igarashi A., Bradham D.M., Okochi H., "Connective tissue growth factor."; J. Dermatol. 19:642-643(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTGE_HUMAN STANDARD; PRT; 349 AA.
P29279; 0960X2;
01-DEC-1992 (Rel. 24, Created)
11-DEC-1992 (Rel. 24, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Connective tissue growth factor precursor (Hypertrophic chondrocyte-specific protein 24).
CTGF OR HCS24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LHUMAN
                                                                                                                                                                                                                                                                                                                      Oemar B.S., Werner A., Garnier J.M., Do D.D., Godoy N., Nauck M Marz W., Rupp J., Pech M., Luescher T.F.;
"Human connective tissue growth factor is expressed in advanced atherosclerotic lesions.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bradham D.M., Igarashi A., Potter R.L., Grotendorst G.R.; "Connective tissue growth factor: a cystelne-rich mitogen secreted human vascular endothelial cells is related to the SRC-induced immediate early gene product CEF-10."; J. Cell Biol. 114:1285-1294(1991).
                                                                                                                                                                                                     TISSUE=Chondrocytes;
MEDLINE=20080284; Pu
                                                                                                                                                                                                                                FUNCTION
                                                                                                                                                                                                                                                                        Cobley
                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                            Circulation
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SOLUBLE FORM (BY SIMILARITY).
ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named
                                      SUBURIT: Monomer.
SUBCELLULAR LOCATION: FOUND IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       357
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (Human).
                                                                                                                                                                                                      PubMed=10614647;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                347
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    isoforms=2;
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Query Match
Best Local :
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Pfam; PF00090; tsp_1; 1
Pfam; PF00093; vwc; 1.
SMART; SM00041; CT; 1.
SMART; SM00121; IB; 1.
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and for entities requires a license agreement (See http://www.isb-sib
                                                                                                                                                                                                                                                                                     SMART; SM00209;
SMART; SM00214;
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InterPro;
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                                                             VARSPLIC
                                                                     CARBOHYD
                                                                                 CARBOHYD
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                                                                                                                                                                         DOMAIN
                                                                                                                                                                                             SIGNAL
                                                                                                                                                                                                       Alternative
                                                                                                                                                                                                                Cell adhesion;
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                                                                                                                                                                                                                                                                                                                                                                                                                    GO:0005578; C:extracellular matrix; GO:0005886; C:plasma membrane; TAS.
GO:0005520; F:insulin-like growth fa GO:00085521; P:cell growth and/or mai GO:0008151; P:epidermal differentiat GO:0009611; P:response to wounding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY: Contains 1 IGFBP domain.
SIMILARITY: Contains 1 VWFC domain.
SIMILARITY: Contains 1 TSP type-1 domain.
SIMILARITY: Contains 1 C-terminal cystine knot-like (CTCK) domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                           PF00007;
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                                                                                                                                                                                                                                 ps01185; CTCK_1; 1.
ps01225; CTCK_2; 1.
ps00222; IGF_BINDING; :
ps50092; TSP1; 1.
ps01208; VMFC_1; 1.
Similarity
                                                                                                                                                                                                                        PS50184; VWFC
                                                                                                                                                                                                                                                                                                                                                         IPR001007; VWF_C. 0007; Cys_knot; 1.
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IPR006207; Cys_knot_C.
IPR000867; Insl_gro_fac_pr.
IPR000884; TSP1.
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                              A,
                                                                                                                                                                                                                DNA synthesis;
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P:epidermal differentiation; TAS.
P:response to wounding; TAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                C:plasma membrane; TAS.
F:insulin-like growth factor binding activity; TAS
                                                                                                                                                                                                                                                                                     VWC; 1
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44.88;
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N-LINKED (GLCNAC...
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/FTIG=VSP_002460.
D -> H (IN REF. 4).
W; 0ECF8470B357EA95 CI
                                                                                       BY SIMILARITY.
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Pred.
                                                                                                                                          CTCK.
         Score 947;
                                                                                                                                                      TSP TYPE-1.
                                                                                                                                                                                    CONNECTIVE
                                                                                                                                                                                                                Extracellular matrix;
 No.
 80
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                                                                                                                                                                                    TISSUE
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ng as its content
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           DB
                                                                                                                                                                                    GROWTH FACTOR
                                                          m Short).
         Length 349;
                              CRC64;
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                                                                     (POTENTIAL).
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Matches

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Mismatches

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RESULT
CTGF_B
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Liliensiek B., Lin Z.,
Kanitz M., Kauffmann G
Submitted (AUG-1997) t
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O18739; Q9GL71;
15-JUL-1998 (Rel. :
28-FEB-2003 (Rel. :
28-FEB-2003 (Rel. :
                                                                    This
                                                                                                          -I- FUNCTION: MAJOR CONNECTIVE TISSUE MITOATTRACTANT SECRETED BY VASCULAR ENCOTHELIAL CELLS. PROMOTES PROLIFERATION AND DIFFERENTIATION OF CHONDROCYTES (BY SIMILARITY). MEDIATES CELL ADHESION AND ENHANCES FIBROBLAST GROWTH FACTOR-INDUCED DNA SYNTHESIS (BY SIMILARITY).
-I- SUBUNIT: MOTOOMER (BY SIMILARITY).
-I- SUBCELLULAR LOCATION: FOUND IN THE EXTRACELLULAR MATRIX AND AS SOLUBLE FORM (BY SIMILARITY).
-I- SUBCELLULAR (CONTAINS 1 IGFBP domain.
-I- SIMILARITY: Contains 1 VMFC domain.
-I- SIMILARITY: Contains 1 TSP type-1 domain.
                                                                                                                                                                                                                                                                                                                                                                                           Mathahs M., Schwitters C., Hove M., Rupp S., Erondu N.E.; Bovine connective tissue growth factor, organization of the chromosomal gene and demonstration of promoter activity."; submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE-Liver;
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NCBI_TaxID=9913;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
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by non-
                                          SWISS-PROT entry is copyright. It is produced through a collaboration en the Swiss Institute of Bioinformatics and the EMBL outstation
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Bioinformatics Institute. The Bioinformatics Institute.
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., Schweigerer L., Ziegler R., Nawro
o the EMBL/GenBank/DDBJ databases.
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Matches 172
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InterPro: IPR006207; Cys_Knot_C.
InterPro: IPR006207; Cys_Knot_C.
InterPro: IPR0008867; Insl_gro_fac_pr.
InterPro: IPR0008867; TSP1.
InterPro: IPR0000884; TSP1.
InterPro: IPR00007; VWF_C.
Pfam; PF00007; Cys_Knot; 1.
Pfam; PF000091; Cys_Knot; 1.
Pfam; PF00093; VWG; 1.
SMART; SM000121; IB; 1.
SMART; SM001021; IB; 1.
SMART; SM00214; VWC; 1.
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ps01225; CTCK_2; 1.
ps00222; IGF_BINDING;
ps002092; TSP1: 1.
ps01208; VWFC_1; 1.
ps01208; VWFC_2; 1.
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                                        STRYTNDNPECRLVKETRICEVRPCGQPVYSSLKKGKKCSKTKKSPEPVRFTYAGCLSVK
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                                                                                                                      VGCVPLCSVDVRLPSPDCPFPRRVKLPGKCCEEWVCDE-----PKEHT--VVGPALAAYR
                                                                                                                                    VGCIPLCPQELSLPNLGCPNPRLYKVTGQCCEEWVCDEDSIKDPMEDQDGLLGKELGFDA
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                         STRVTNDNAFCRLEKQSRLCMVRPCEADLEENIKKGKKCIRTPKISKPIKFELSGCTSMK
                                                                                              SEVELTRNNELIAVGKGRSLKRLPVFGMEPRILYNPLQGQKCIVQTTSWSQCSKTCGTGI
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MISSING (IN REF. 1).
A -> T (IN REF. 1).
CV -> YI (IN REF. 1).
CDEP -> SRDE (IN REF.
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BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
D -> DC (IN REF
                                                                                                                                                                                                                                                                  Score 933; DB
Pred. No. 8.5e
59; Mismatches
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RESULT 9
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   PROSITE; PS0118
PROSITE; PS0122
PROSITE; PS0022
PROSITE; PS5009
PROSITE; PS50120
PROSITE; PS5018
Cell adhesion;
                                                                                                                                             SMART;
SMART;
SMART;
                                                                                                                                                                                                                    Pfam;
Pfam;
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between
the Euro
                                                                                                                                                                                                                                                                                                                                                                                                   use by non-profit institutions as long modified and this statement is not removed entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Purification and characterization of novel heparin-binding grow factors in uterine secretory fluids. Identification as heparin-regulated Mr 10,000 forms of connective tissue growth factor.", J. Biol. Chem. 27:20275-20282(1997).

-I- FUNCTION: MAJOR CONNECTIVE TISSUE MITOATTRACTANT SECRETED BY VASCULAR ENDOTHELIAL CELLS. PROMOTES POLIFERATION AND DIFFERENTIATION OF CHONDROCTES (BY SIMILARITY). MEDIATES CE ADHESION AND ENHANCES FIBROBLAST GROWTH FACTOR-INDUCED DNA SYNTHESIS (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sus scrofa (Pig).
Eukaryota; Metazoa;
Mammalia; Eutheria;
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019113;
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15-UUL-1998 (Rel. 36, Last sequence update
28-FEB-2003 (Rel. 41, Last annotation update
Connective tissue growth factor precursor.
                                                                                                                                                                                                                                                                                                                                                  InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SYNTHESIS (BY SIMILARITY).

SYNTHESIS (BY SIMILARITY).

SUBUNIT: MONOMER (By SiMILARITY).

SUBCELLULAR LOCATION: FOUND IN THE EXTRACELLULAR MATRIX AND AS A SUBUBLE FORM (BY SIMILARITY).

SIMILARITY: Contains 1 IGFBP domain.

SIMILARITY: Contains 1 VWFC domain.

SIMILARITY: Contains 1 TSP type-1 domain.

SIMILARITY: Contains 1 C-terminal cystine knot-like (CTCK) domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
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PF00090;
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                                                                                                                                                                                                       PF00093;
                                                                                                                                                                                                                                                      PF00007; Cys_knot;
                                                                                                                              SM00041;
SM00121;
SM00209;
SM00214;
                  2; PS01185; CTCK_1; 1.
2; PS01225; CTCK_2; 1.
2; PS00222; IGF_BINDING; 1.
2; PS50092; TSP1; 1.
2; PS01208; VWFC_1; 1.
2; PS50184; VWFC_2; 1.
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o; IPR006207; Cys_knot_C.
o; IPR000867; Insl_gro_fac_pr.
o; IPR000864; Tspl.
o; IPR001007; VWF_C.
pr00007; Cys_knot; 1.
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Cetartiodactyla; Suina; Suidae;
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 Extracellular matrix; Signal.
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                                                                                    nephroblastomas.";

MOI. Cell. Biol. 12:10-21(1992).

-i-FUNCTION: IMMEDIATE-EARLY PROTEIN LIKELY TO PLAY A ROLL

-i-GROWTH REGULATION. ITS OVEREXPRESSION IS ASSOCIATED WIT

TUMORIGENESIS AND EXPRESSION OF A N-TERMINAL-TRUNCATED
                                                                                                                                           STRAIN-Brown leghorn;
MEDLINE-92107157; PubMed-1309586;
Joliot V., Martinerie C., Dambrin
                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                        P28686;
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01-DEC-1992
01-DEC-1992
28-FEB-2003
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CHAIN
NCBI_TaxID=9031;
                      Archosauria;
                                 Eukaryota;
                                          Gallus gallus (Chicken).
                                                                 NOV protein
                                                                                                                          NOV_CHICK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        il Similarity
167; Conserv
                                                                                                                                                                                                                                                                                      ISTRVTNDNPECRLYKETRICEVRPCGQPVYSSLKKGKKCSKTKKSPEPVRFTYAGCLSV
                                                                                                                                                                                                                                                                                                                                                                                                                          QPCDHTKGLECNEGASSTALKGICRAQSEGRPCEYNSRIYQNGESFQPNCQHQCTCIDGA
                                                                                                                                                                                   ESLYYRKMYGDM
                                                                                                                                                                                                        FPFY--RLFNDI
                                                                                                                                                                                                                                                   KKYRPKYCGSCVDGRCCTPQLTRTVKMRFRCEDGETFSKNVMMIQSCKCNYNCPHANEAA
                                                                                                                                                                                                                                                                                                                                  VGCIPLCPQELSLPNLGCPNPRLVKYTGQCCEEWVCDEDSIKDPMEDQDGLLGKELGFDA
                                                                                                                                                                                                                                                                                                                                                                                                              DPCDPHKGLFCDFGSPANRKIGVCTAK-DGAPCVFGGTVYRSGESFQSSCKYQCTCLDGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                           AFVLLLALCSRPASGQDCSGQCQCAAGKRRACPAGVSLVLDGCGCCRLCAKQLGELCTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ALVVTLLHLTRLAL-STCPAACHCPL-EAPKCAPGVGLVRDGCGCCKVCAKQLNEDCSKT
                                                                                                                                                                                                                              KTYRAKFCGVCTDGRCCTPHRTTTLPVEFKCPDGEVMKKSMMFIKTCACHYNCPGDNDIF
                                                                                                                                                                                                                                                                          ISTRVTNDNAFCRLEKQSRLCMVRPCEADLEENIKKGKKCIRTPKISKPVKFELSGCTSV
                                                                                                                                                                                                                                                                                                                                                                  VGCVPLCSMDVRLPSPDCPFPRRVKLPGKCCEEWVCDEP----
                                 Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (Rel. 24, Created)
(Rel. 24, Last sequence up
(Rel. 41, Last annotation
precursor (Nephroblastoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                       Aves;
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                                                                                                                           STANDARD;
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                      Neognathae;
                                 Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  42.8%;
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CTCK.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. 7.7e7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 906;
Pred. No. 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IGFBP.
                      Craniata; Ver; Galliformes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CONNECTIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL.
                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BB510E2B2B52D4A0
                                                                                           update)
                                                                                                                            351
                                                                  update)
overexpressed
                      Vertebrata; Euteleostomi;
mes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .7e-59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1;
                                                                                                                           ΑA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        108;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CRC64;
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                                                                  gene
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                                                                  protein).
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Dambrine

G.,

Plassiart

G.,

Brisac

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gene

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CELL

VERSION

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Query Match
Best Local S
Matches 164
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Pfam; PF00093; vwc; 1.
SMART; SM00041; CT; 1.
SMART; SM00121; IB; 1.
SMART; SM00209; TSP1; 1
SMART; SM00214; VWC; 1.
                                                                                                                                                                                         DISULFID DISULFID DISULFID DISULFID DISULFID CARBOHYD
                                                                                                                                                                                                                                                                                                                                                              PROSITE;
PROSITE;
PROSITE;
PROSITE;
                                                                                                                                                                                                                                                                                  DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                         PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the El the European Bioinformatics Institute. There are no resti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00007; Cys_knot; Pfam; PF00219; IGFBP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR006208; Cys_knot.
InterPro; IPR006207; Cys_knot_C.
InterPro; IPR000867; Insl_gro_fac_pr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        entities requires
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                         CHAIN
                                                                                                                                                                                                                                                                                                                    SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            or send an email to license@isb-sib.ch).
                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                Proto-oncogene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              [nterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY: Contains 1 IGFBP domain.
SIMILARITY: Contains 1 VWFC domain.
SIMILARITY: Contains 1 TSP type-1 domain.
SIMILARITY: Contains 1 C-terminal cystine knot-like (CTCK)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OF NOV GENE IN CHICKEN EMBRYONIC FIBROBLASTS (CEF) IS SUFFICIENT TO INDUCE THE TRANSFORMATION OF CEF IN VITRO.
SUBCELLULAR LOCATION: Secreted.
TISSUE SPECIFICITY: BRAIN AND HEART, AND AT A LOWER LEVEL IN MUSCLE AND INTESTINE, IN THE EMBRYO. LUNG AND LESS SO IN BRAIN A MUSCLE AND INTESTINE. IN THE EMBRYO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DEVELOPMENTAL STAGE: MAV1-INDUCED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MUSCLE AND INTESTINE, IN SPLEEN, IN ADULT CHICKEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADULT KIDNEY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LEVEL OF NOV GENE WHOSE TRANSCRIPTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           S20078;
131
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                                           72
                                                                  65
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                                                                                                                                               Similarity
                                                                                                               LVVTLLHLTRLALS----TCPAAC--HCPLEAPKCAPGVGLVRDGCGCCKVCAKQLNEDC
                                                                                        PS00222;
DGQIGCLPRCNLGLLLPGPDCPFPRKIEVPGECCEKWVC
                     DGAVGCIPLCPQELSLPNLGCPNPRLVKVTGQCCEEWVCDEDSIKDPMEDQDGLLG----
                                           SPLLPCDESGGLYCDRGPEDGGGAGICMV-LEGDNCVFDGMIYRNGETFQPSCKYQCTCR
                                                                  SKTQPCDHTKGLECNFGASSTALKGICRAQSEGRPCEYNSRIYQNGESFQPNCQHQCTCI 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IPR000884; TSP1.
IPR001007; VWF_C.
                                                                                                                                                                                351 AA;
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31
104
201
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258
275
286
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                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                Growth
                                                                                                                                                                                                                                                                                                                                         IGF_BINDING;
TSP1; 1.
VWFC_1; 1.
; VWFC_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                     CTCK_1; 1.
CTCK_2; 1.
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                                                                                                                                            40.2%;
                                                                                                                                                                                38268
                                                                                                                                                                                MW;
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                                                                                                                                                                             TSP TYPE-1.
CTCK.
BY SIMILARITY.
N-LINKED (GLCWAC.
W; 1ECB3FA3058C6797 C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        agreement
                                                                                                                                               Score 851.5;
Pred. No. 6.
                                                                                                                                                                                                                                                                                                        POTENTIAL.
                                                                                                                                                                                                                                                                                            IGFBP.
                                                                                                                                                                                                                                                                                                                                Signal.
                                                                                                                                     Mismatches
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TION IS NORMALLY
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                                                                                                                                             .9e-55;
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                                                                                                                                                            DB
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                                                                                                                                     104;
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                                                                                                                                                         1;
                                                                                                                                                                                 CRC64;
                                                                                                                                                        Length 351;
                                                                                                                                     Indels
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                                                                                                                                                                                            (POTENTIAL)
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 -DPRDEV - -LLGGFAM
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                                                                                                                                     61;
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                                                                                                                                     Gaps
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RESULT 11
NOV_COTJA
                                                                                                                       Pfam; PF00219; IĞFBP; 1
Pfam; PF00090; tsp_1; 1
Pfam; PF00093; vwc; 1
SMART; SM00041; CT; 1
SMART; SM00121; IB; 1.
SMART; SM00219; TSP1; 1
SMART; SM00214; VWC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P42642;
01-NOV-1995
           PROSITE;
PROSITE;
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PROSITE;
PROSITE;
                                                                                                                                                                                                                                                   InterPro; IPR006208; Cys_knot.
InterPro; IPR006207; Cys_knot_C.
InterPro; IPR000867; Insl_gro_fac_pr.
InterPro; IPR000884; TSP1.
InterPro; IPR001007; VWF_C.
Pfam; PF00007; Cys_knot; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Me
Archosauria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Coturnix coturnix japonica (J. Eukaryota; Metazoa; Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VOV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1995
28-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                   entities requires a license agreement (S or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                               EMBL; U13063;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            <del>'</del>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Weiskirchen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=93934;
Proto-oncogene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBCELLULAR LOCATION: Secreted (By similarity).
SIMILARITY: Contains 1 IGFBP domain.
SIMILARITY: Contains 1 VWFC domain.
SIMILARITY: Contains 1 TSP type-1 domain.
SIMILARITY: Contains 1 C-terminal cystine knot-like (CTCK) domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            skirchen R., Bister mitted (AUG-1994) to FUNCTION: IMMEDIATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mitted (AUG-1994) to the EMBL/GenBank/DDBJ databases FUNCTION: IMMEDIATE-EARLY PROTEIN LIKELY TO PLAY A GROWTH REGULATION (BY SIMILARITY).
SUBCELLULAR LOCATION: Secreted (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                327
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                                                                                                                                                                                                                                                                                                                                                                                                                                     non-profit institutions as long and this statement is not removed.
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                                                                                       PS012
                                                                                                                                                                                                                                                                                                                                                                                                                      requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AVRFEYKNCTSVQTYKPRYCGLCNDGRCCTPHNTKTIQVEFRCPQGKFLKKPMMLINTCV
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                                                                        PS0027
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                                                                                                                                                                                                                                                                                                                                                                   AAA21128.1;
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Growth
                 ; TSP1; 1.
; VWFC_1; 1.
; VWFC_2; 1.
                                                                        IGF_BINDING;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Neognathae; Galliformes; Phasianidae; Phasianinae;
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Last annotation updat
(Nephroblastoma overe
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factor;
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ta; Craniata; Vert
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Signal
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Query Match
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Matches 164
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P48745; Q96BY5;
O1-FEB-1996 (Re
O1-FEB-1996 (Re
15-SEP-2003 (Re
                                                                                                                                                                                                                                                                                                                                                                                   HUMAN
                                               MEDLINE=94336229; PubMed=7520150; Martinerie C., Huff V., Joubert I Strong L.C., Perbal B.; "Structural analysis of the human in Wilms tumor."; Oncogene 9:2729-2732(1994).
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DISULFID
DISULFID
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CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
DOMAIN
SEQUENCE FROM N.A. Jiang D., Gou D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CHAIN
                                                                                                                                                                                        Mammalia; Eutheria; NCBI_TaxID=9606;
                                                                                                                                             TISSUE=Placenta;
                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                         Eukaryota;
Mammalia; |
                                                                                                                                                                                                                                                                   gene protein
                                                                                                                                                                                                                       Homo sapiens (Human)
Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                       NOV protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HQCTCIDGAVGCIPLCPQELSLPNLGCPNPRLVKVTGQCCEEWVCDEDSIKDPMEDQDGL 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ALVVTLLHLTRLAL------STCPAAC--HCPLEAPKCAPGVGLVRDGCGCCKVCAK 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MIQSCKCNYNCPHANEAAF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CIEQTTEWSACSRSCGMGFSTRVTNRNQQCEMVKQTRLCMMRPCENEEPSD-KKGKKCIR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LGGFAMAAYRQEATLGIDVSD---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SLPVLLLLLLLLRPSEVNGREAPCPRPCGGRCPAEPPRCAPGVPAVLDGCGCCLVCAR
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(Rel. 33, Last sequence up
(Rel. 42, Last annotation
                                                                                                                                                                                                                                                                                     homolog
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                                                                                                                                                                                                                                                                   homolog).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AA,
   Li W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26
353
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                                                                                                                                                                                                       Chordata;
Primates;
                                                                                                                                                                                                                                                                                  precursor (NovH) (Nephroblastoma overexpressed
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43.3%;
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CTCK.
EY SIMILARITY.
BY 
                                                                               human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            367
                                                                                                                                                                                                                                                                                                                                                                                                                                             341
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                                                                                                                                                                                                       Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL.
NOV PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                   PRT;
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                                                                                                            Η.,
                                                                               nov
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                                                                                                            Badzioch M.,
                                                                                                                                                                                                                                                                                                                                                                   357
                                                                            proto-oncogene and expression
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.2e-54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length
                                                                                                            Saunders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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                                                                                                            G.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   66;
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 InterPro; IPR006208; Cys_k
InterPro; IPR006207; Cys_k
InterPro; IPR000867; Insl_
InterPro; IPR000884; TSP1_
InterPro; IPR001007; VWF__
Pfam; PF00007; Cys_knot; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STROMAL TYPE.
-!- SIMILARITY: Co
-!- SIMILARITY: Co
-!- SIMILARITY: Co
                                                                                                                                                                                                                                                                                                                                                                                                             This SWI
between
                                                                                                                                                                                                    EMBL;
                                                                                                                                                                                        PIR;
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Submitted
                                                                                                                                                           MIM; 164958;
                                                                                                                                                                        Genew;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- SIMILARITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PubMed=9927660;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INTERACTION WITH FBLN1.
                                                                                                                                                                                                    X78351; CAA55146.1;

X78352; CAA55146.1;

X78353; CAA55146.1;

X78354; CAA55146.1;

X78354; CAA65403.1;

X96584; CAA65403.1;

AY082381; AAL92490.1

BC015028; AAH15028.1
                                                                                                                                                                                     138069;
                                PF00090;
                                                                                                                                                                   HGNC:7885;
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                                                                                                                                                                                        I38069
tsp_1;
vwc; 1;
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                                           IGFBP;
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                                                             VWF_C.
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RA Strausberg R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altasher R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altasher R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altasher R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altasher R.E., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Hopkins R.E., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Raha S.S., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hullyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hullyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hullyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hullyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hullyk S.W.,
RA Raha S.J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Willalon D.K., Marna M., Schmet S.J., W., Bouffard G.G.,
RA Butkersley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Butkersley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.",
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Perbal B., Martinerie C., Sainson R., Werner M.,
"The C-terminal domain of the regulatory protein
promote interaction with fibulin IC: a clue for a
cell-adhesion signaling.";
Proc. Natl. Acad. Sci. U.S.A. 96:869-874(1999).
-1- FUNCTION: IMMEDIATE-BARLY PROTEIN LIKELY TO P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    use by non-profit institutions as long as its cont modified and this statement is not removed. Usage by entities requires a license agreement (See http://www.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produbetween the Swiss Institute of Bioinformatics the European Bioinformatics Institute. There \varepsilon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        or send an email to license@isb-sib.ch).
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SUBUNIT: Interacts with FELMI.
SUBCELLULAR LOCATION: Secreted.
TISSUE SPECIFICITY: INCREASED EXPRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contains 1 IGPBP domain.
Contains 1 VWFC domain.
Contains 1 TSP type-1 domain.
Contains 1 C-terminal cystine knot-like (CTCK) domain.
Insl_gro_fac_pr
                                      Cys_knot_C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and expression of human nov gene."; to the EMBL/GenBank/DDBJ databases.
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JOINED.
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RESULT
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IDV_XEN
IDV P!
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DT 0
DT 2
DT 2
DT 2
OC
OC
OC
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PROSITE; PS01225; C
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CONFLICT
SEQUENCE
                  Eukaryota; Me
Amphibia; Bat
Xenopodinae;
                                                                                                                  NOV_XENLA
P51609;
01-OCT-1996
01-OCT-1996
28-FEB-2003
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157; Conser
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SM00209; TSP1; 1
SM00214; VWC; 1.
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                    Batrachia; Anura;
ae; Xenopus.
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3 (Rel. 41, Last anno
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CTCK_2; 1.
CTCK_2; 1.
IGF_BINDING;
TSP1; 1.
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VWFC_2;

    Last sequence up
1, Last annotation
precursor (Xnov).

                                                      Chordata;
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43.1%;
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VWFC.

TSP TYPE-1.

TSP TYPE-1.

GTCK.

BY SIMILARITY.

                                    a; Craniata; Ve:
Mesobatrachia;
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3; Mismatches
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                                                                    frog)
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                                                      Vertebrata; Euteleostomi;
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Best Local S
Matches 158
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InterPro; IPR006207; Cys_knot_C.
InterPro; IPR006207; Cys_knot_C.
InterPro; IPR000867; Insl_gro_fac_pr.
InterPro; IPR000884; TSP1.
InterPro; IPR001007; VWF_C.
Pfam; PF00007; Cys_knot; 1.
Pfam; PF000219; IGFBP; 1.
Pfam; PF00093; VWG; 1.
Pfam; PF00093; VWG; 1.
SMART; SM00041; CT; 1.
SMART; SM00214; VWG; 1.
SMART; SM00214; VWG; 1.
SMART; SM00214; VWG; 1.
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"Isolation and characterization of xnov,
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SEQUENCE FROM N.A
MEDLINE=96257227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; U37063; AAB17096.1;
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SUBCELLULAR LOCATION: Secreted.
SIMILARITY: Contains 1 IGFBP domain.
SIMILARITY: Contains 1 VWFC domain.
SIMILARITY: Contains 1 TSP type-1 domain.
SIMILARITY: Contains 1 C-terminal cystine knot-like (CTCK)
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e 171:243-248(1996)
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PS00222;
PS50092;
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                  VGCIPLCPQELSLPNLGCPNPRLVKVTGQCCEEWVCDEDSIKDPMEDQDGLLG-----
                                                QPCDHTKGLECNFGASSTALKGICRAQSEGRPCEYNSRIYQNGESFQPNCQHQCTCIDGA
                                                                                         LALVVTLLHLTRLALSTCPAAC-HCPLEAPKCAPGVGLVRDGCGCCKVCAKQLNEDCSKT
                                                                             LALCFILL-IQQVASQKCPSQCDQCPEEPPSCAPSVLLILDGCGCCPVCARQEGESCSHL
IGCVPRCNLDLLLPGPDCPFPRRVKVPGECCEKWVCDS---
                                      NPCQEDKGLYCEFNADPRMETGTCMA-LEGNSCVFDGVVYRNRESFQPSCKYHCTCLNGH
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41.8%;
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CTCK.
BY SIMILARITY.
N-LINKED (GLCNAC.
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Pred. No. 5.2
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NOV PROTEIN
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MBL outstation -
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15-SEP-2003
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EMBL;
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MGD; N
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Oncogene 12:1479-1492(1996).
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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01-NOV-1997
                                                                                                                                                                                                                                                                                                                   between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Martinerie C., Chevalier G., 
"Regulation of nov by WT1: a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=C57BL/6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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                                           InterPro;
                                                                nterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=96204003; PubMed=8622864;
                                                                                     :; X97863; CAA66457
L; Y09257; CAA70454
L; X96585; CAA65404
; MGI:109185; NOV.
                                                                                                                                                                                                                                                                                       European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                          SUBUNIT: Interacts with FBLN1 (By similarity).
SUBCELULAR LOCATION: Secreted.
SIMILARITY: Contains 1 IGFBP domain.
SIMILARITY: Contains 1 VWFC domain.
SIMILARITY: Contains 1 TSP type-1 domain.
SIMILARITY: Contains 1 C-terminal cystine knot-like (CTCK)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GROWTH REGULATION (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FUNCTION:
                                                                                                                                                                                                                                                                                                         SWISS-PROT entry is copyright. It is produced through a collaboration en the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                320
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                                                                                                                                                                                                 requires a license agreement (See http://www.isb-sib.an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RFTYAGCLSVKKYRPKYCGSCVDGRCCTPQLTRTVKMRFRCEDGETFSKNVMMIQSCKCN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QCSKTCGTGISTRVTNDNPECRLVKETRICEVRPC-GQPYYSSLKKGKKCSKTKKSPEPV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ---KELGFDASEVELTRNNELIAVGKGRSLKRLPVFGMEPRILYNPLQGQKCIVQTTSWS
IPR006208; Cys_knot:
    IPR006207; Cys_knot_C.
    IPR000867; Insl_gro_fac_pr.
    IPR000884; TSP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (Rel. 35, Created)
(Rel. 35, Last sequence update)
(Rel. 42, Last annotation updat
homolog precursor (NovH) (Nephr
                                                                                                          ; CAA66457.1; -.; CAA70454.1; -.; CAA65404.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                homolog).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     potential role
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rauscher F.J.
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Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     notation update)
(NovH) (Nephroblastoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Vertebrata; I
thi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Choi C.P.,
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Murinae; Mus
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Best Local S
Matches 162
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Pfam; PF00093; vwc; 1.
SMART; SM00041; CT; 1.
SMART; SM00121; IB; 1.
SMART; SM00209; TSP1; 1
SMART; SM00214; VWC; 1.
                 NOV_RAT
Q9QZQ5;
28-FEB-2003
28-FEB-2003
15-SEP-2003
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DOMAIN
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gene
         NOV protein
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PF00219;
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                                                                                                                                                                                                                                                                                                                                                                                                 162;
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                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                            NNEA
                                                                                                                                                               GCLSVKKYRPKYCGSCVDGRCCTPQLTRTVKMRFRCEDGETFSKNVMMIQSCKCNYNCPH
                                                                                                                                                                                                                                                                                  CIDGAVGCIPLCPQELSLPNLGCPNPRLVKVTGQCCEEWVCDEDSIKDPMEDQDGLLGKE
                                                                                                                                                                                                                                                                                                                          DCSKTQPCDHTKGLECNFGASSTALKGICRAQSEGRPCEYNSRIYQNGESFQPNCQHQCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PS50184; VWFC_2;
                                                                                                                                 ANEA
                                                                                                                                                                                                    CGTGISTRVTNDNPECRLVKETRICEVRPCGQ-PVYSSLKKGKKCSKTKKSPEPVRFTYA
                                                                                                                                                                                                                                                                         CRDGQIGCLPRCQLDVLLPGPDCPAPRKVAVPGECCEKWTCGSDE----
                                                                                                                                                                                                                                                                                                                                                                        RALALVVTILH-LTRLALS-TCPAAC--+HCPLEAPKCAPGVGLVRDGCGCCKVCAKQLNE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PS01225; CTCK_2;
                                                                                                                                                                                           CGMGVSTRVTNRNRQCEMVKQTRLCIVRPCEQEPEEVTDKKGKKCLRTKKSLKAIHLQFE
                                                                                                                                                                                                                                  LALPAYRPEAT - - - - -
                                                                                                                                                                                                                                                                                                                SCSEMRPCDQSSGLYCDRSADPNNQTGICMV-PEGDNCVFDGVIYRNGEKFEPNCQYFCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PS00222;
                                                                                                                                                   NCTSLYTYKPRFCGVCSDGRCCTPHNTKTIQVEFQCLPGEIIKKPVMVIGTCTCYSNCPQ
                                                                                                                                                                                                                                              RCLCLGFLLFHLLSQVSASLRCPSRCPPKCPSISPTCAPGVRSVLDGCSCCPVCARQRGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IPR001007; VWF_
                                                                                                                                                                                                                                                                                                                                                                                                                                     277
354
        (Rel. 41, Created)
(Rel. 41, Last sequence update)
(Rel. 42, Last annotation updat
homolog precursor (NovH) (Nephr
                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                365
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IGFBP; 1.
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                                                            STANDARD;
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; TSP1; 1.
; VWFC_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CTCK_1;
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354
101
168
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334
         precursor (NovH) (Nephroblastoma
                                                                                                                                                                                                                                                                                                                                                                                                                                        38928
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CTCK.
CTCK.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
OBJURT (GLUNGC. . .) (POTENTIAL).
N-LINKED (GLUNGC. . .) (POTENTIAL).
N-LINKED (GLUNGC. . .) (POTENTIAL).
N-LINKED (GLUNGC. . .) (POTENTIAL).
N-LINKED (GLUNGC. . .) (POTENTIAL).
N-LINKED (GLUNGC. . .) (POTENTIAL).
                                                                                                                                                                                                                                 -VGVEVSDSSI----
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                                                                                                                                                                                                                                                                                                                                                                                               Score 822; DB
Pred. No. 9.5e
16; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL..
NOV PROTEIN HOMOLOG.
IGFBP.
VWFC.
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2 9.
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                    update)
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Rattus norvegicus

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Query Match
   Matches
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InterPro; IPR006207; Cys_knot_C.
InterPro; IPR006207; Insl_gro_fac_pr.
InterPro; IPR000867; Insl_gro_fac_pr.
InterPro; IPR001007; VWF_C.
Pfam; PF00007; Cys_knot; 1.
Pfam; PF000219; IGFBP; 1.
Pfam; PF00099; tsp_1; 1.
                                                                                                                                                                                                                                 PROSITE: PSO0125; CTCK_1; 1.
PROSITE: PS01225; CTCK_2; 1.
PROSITE: PS00222; IGF_BINDING; 1
PROSITE: PS50092; TSP1; 1.
PROSITE: PS50184; VWFC_1; 1.
PROSITE: PS50184; VWFC_2; 1.
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PROSITE;
PROSITE;
                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                     SIGNAL
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MEDLINE-20035752; PubMed-10570975;
Liu C., Liu X.J., Crowe P.D., Kelner G.S.,
Ling N., De Souza E.B., Maki R.A.;
                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/an
                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                             Growth
                                                                                                                                                                                                                                                                                                                            SMART;
                                                                                                                                                                                                                                                                                                                                          SMART;
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                                                                                                                                                                                                                                                                                                                                                                  Ptam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AF171936; AAD49371.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               between the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Nephroblastoma overexpressed gene (NOV) codes for that induces protein tyrosine phosphorylation."; Gene 238:471-478(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A., AND CHARACTERIZATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rattus norvegicus (Rat).
Eukaryota, Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
               Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Protein.
SUBUNIT: Interacts with FBLN1 (By similarity).
SUBCELLULAR LOCATION: Secreted.
TISSUE SPECIFICITY: Ubiquitous.
SIMILARITY: Contains 1 IGFBP domain.
SIMILARITY: Contains 1 TSP type-1 domain.
SIMILARITY: Contains 1 TSP type-1 domain.
SIMILARITY: Contains 1 TSP type-1 domain.
                                                                                                                                                                                                                                                                                                                                     1; PF00090; tsp_1;
1; PF00093; vwc; 1.
2T; SM00041; CT; 1.
2T; SM00121; IB; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FUNCTION: Can act as a growth factor for some cells and binds to specific receptor that leads to the phosphorylation of a 221\ \mathrm{kDa}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
   158;
                                                                                                                                                                                                                                                                                                               SM00121; IB; 1.
SM00209; TSP1; 1
SM00214; VWC; 1.
                                                                                                                                                                                                                             factor;
              Similarity
   Conservative
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                                                   A,
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CHARGE (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
MW; 02619707DE7C1BFB CRC64;
Score 818.5; DB 1;
Pred. No. 1.7e-52;
9; Mismatches 118;
                                                                                                                                                              VWFC.
TSP TYPE-1.
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NOV PROTEIN HOMOLOG.
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Sciurognathi; Muridae;
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                                                               GCLSVKKYRPKYCGSCVDGRCCTPQLTRTVKMRFRCEDGETFSKNVMMIQSCKCNYNCPH 361
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                                                                                                                    CGTGISTRVINDNPECKLVKETRICEVRPCGQ-PVYSSLKKGKKCSKTKKSPEPVRFTYA 301
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Search completed: Job time: 10.525 August 5 2003, 14:05:37

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Result
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Maximum DB
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Copyright (c) 1993 - 2003 Compugen Ltd.
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2971.515 Million cell updates/sec
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Q9wtm9 rattus norv
Q99ktx5 xenopus lae
Q9uid7 homo sapien
Q42607 xenopus lae
Q98tq8 gallus gall
Q9pt80 notophthalm
Q97765 sus scrofa
Q8ca67 mus musculu
Q95238 homo sapien
Q99pp0 rattus norv
Q54775 mus musculu
Q95238 homo sapien
Q8cic8 mus musculu
Q9hcs3 homo sapien
Q9pss6 gallus gall
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7.5	7.5	159 7.5 5	7.5	7.5	7.6	7.6	.5 7.6	7.7	7.8	7.9	8.0	8.0	169 8.0 1	8.1	8.2	8.2	8.2	8.3	8.8	9.2	13.8	13.9	w	15.9	15.9	15.9	16.1	17.7
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ALIGNMENTS

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Signal.	 PROSITE: PS01208: VWFC: 1.	1000000	· pesonos.	PROSITE; PS00222; IGF_BINDING; 1.	1001110	PROSTTE: PS01225: CTCK 2: 1.	FROSTIE, FOOTIOO, CICALI, I.	DC01195.	SMART; SM00214; VWC; 1.	CHICOROL,	SM00209:	SMART; SMOULZI; IB; I.		SMART: SM00041: CT: 1.	Fram; Froody3; vwc; 1.	1	Pfam; PF00090; tsp 1; 1.	Ptam; PrOUZ19; IGEBP; 1.	FF 000007,	DE00007. Care ka	InterPro: IPR001007; VWF C.	. interPro; iPROUU884; TSP1.	HTX000007;	TBB000867.	InterPro; IPR006207; Cys_knot_C.	InterPro; IPR006208; Cys_knot.	EMBL; AB015877; BAA78339.1;		ATTINI-1998) to the EMBI	1 mRNA.";	Unoki H., Yonekura H., Furukawa K., Yamamoto H.;	STRAIN-Izm; TISSUE-Aorta;	SECUENCE FROM N.A.			Rodentia; Sciurognathi; Muridae;	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	Rattus norvegicus (Rat).	CTR61	CIRCL PLECUISOI.	programmer. so, base	(Tremaine) 23. Last	(TrEMBLrel.	01-NOV-1999 (TrEMBLrel. 12, Created)	Q9WTM9;	Q9WTM9 PRELIMINARY; PRT; 379 AA.	

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                                                                                                                                                                                                                                                                                                                          "Characterization of Xenopus cyr61.";
Submitted (NOV-2000) to the EMBL/GenBank/DDBJ da
EMBL; AF320592; AAK00947.1; -
InterPro; IPR006208; Cys_knot.
InterPro; IPR006207; Cys_knot.
InterPro; IPR000867; Insl_gro_fac_pr.
InterPro; IPR000884; TSp1.
InterPro; IPR001007; VWF_C.
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Q1-JUN-2001 (TrEMBLrel. 17, Created)
Q1-JUN-2001 (TrEMBLrel. 17, Last sequence update)
Q1-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Q1-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Secreted cysteine-rich protein cyr61.
Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eukaryota; Metazoa; Chordata; Craniata; Pipoidea; Pixenopodinae; Xenopus.
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pixenopodinae; Xenopus.
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Best Local
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                                               SMART; SM
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CHAIN
rtam; PF00219; CYs_knot; 1

rfam; PF00219; IGFBP; 1

rfam; PF00090; tsp_1; 1.

fam; PF00093; vwc; 1

fART; SM000121; IB; 1

RT; SM000121; IB; 1

RT; SM00209; TSP1; 1

TE; PS01185; CTCK_1; 1.

TE; PS01225; CTCK_2; 1

VE; PS00222; IGF_BINDING; 1.

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Pred. No. 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 11;
2.8e-179;
nes 19;
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Best Local 9
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                                          PROSITE;
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PROSITE;
SEQUENCE
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01-MAR-2003
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InterPro: IPR001007; VWF_C
Pfam; PF00007; Cyg_knot; 1
Pfam; PF000219; IGFBP; 1
Pfam; PF00090; tsp_1; 1.
Pfam; PF00090; vwc; 1
Pfam; PF00093; VWC; 1
SMART; SM00041; CT; 1.
SMART; SM00204; TSP1; 1.
SMART; SM00214; VWC; 1.
                                                                                                                                                                                                                      Anding B., Long Y.;
"Cloning of a new gene down-regulated in the sembryonal-rhabdomyosarcoma (RMS).";
Submitted (MAY-1997) to the EMBL/GenBank/DDBJ EMBL; AF003114; AAF21597.1;
                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS01208; VWFC; 1. SEQUENCE 375 AA; 41460 MW;
                                                                                                                                                                InterPro; IPR006208; Cys_knot.
InterPro; IPR006207; Cys_knot_C.
InterPro; IPR000867; Insl_gro_fac_pr.
InterPro; IPR000884; TSP1.
                                                                                                                                                                                                                                                                                           TISSUE=Kidney;
                                                                                                                                                                                                                                                                                                        SEQUENCE OF 1-107 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                    CYR61 protein.
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            PS01225; CTCK_2; 1.
PS50092; TSP1; 1.
PS01208; VWFC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YRLFNDIHKFRD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GELTRKNEFVAVIKG-GLKMLPVFGSDPQ--SHVVENSKCIVQTTSWSQCSKTCGTGIST
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) (TrEMBLrel.
) (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
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37246
                                                                                                                                       VWF_C.
not; 1.
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79.3%;
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Last sequences
Last anno
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Pred. No. 1.5
                                                                                                                                                                                                                                                                                                                                              Craniata; Vo
Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
9188987A7352E948 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                sequence update) annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       334
                                                                                                                                                                                                                                                                                                                                                              Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5; DB 13;
.5e-153;
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                                                                                                                                                                                                                                                                                                                                                Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                  update)
                                                                                                                                                                                                                                                                 small-cell tumor
                                                                                                                                                                                                                                       databases
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                                                                                                                                                                                                                                                                                                                                                              Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                 Homo.
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Best Local S
Matches 295
                                                    Query Match
Best Local (
                                    Matches
                                                                                                                                                                             InterPro; IPRO06208; Cys_knot.
InterPro; IPRO06207; Cys_knot_C.
InterPro; IPRO06207; Cys_knot_C.
InterPro; IPRO00867; Insl_gro_fac_pr.
InterPro; IPRO00867; Tspl.
InterPro; IPRO01007; VWF_C.
Pfam; PF00007; Cys_knot; 1.
Pfam; PF00219; IGFBP; 1.
Pfam; PF00219; IGFBP; 1.
Pfam; PF00203; vwc; 1.
SMART; SM00041; CT; 1.
SMART; SM000209; TSP1; 1.
SMART; SM001214; VWC; 1.
SMART; SM001214; VWC; 1.
                                                                                                                   PROSITE;
PROSITE;
PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                              Ying Z., King M.L.;
Submitted (AUG-1997) to the EMBL/GenBank/DDBJ EMBL; U43524; AAB67639.1; -
EMBL; U43523; AAB67638 1
Interpr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               042607
042607;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Connective tissue growth factor XCTGF.
                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Ven
Amphibia; Batrachia; Anura; Mesobatrachia;
                                                                                                                                                                      PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           xenopodinae; Xenopus.
NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Xenopodinae;
                                                  Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  342
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                                 il Similarity
168; Conserv
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                                                                                                   PS01208;
343 AA;
                                                                                                                                   PS01225;
PS50092;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NGESFQPNCQHQCTCIDGAVGCIPLCPQELSLPNLGCPNPRLVKVTGQCCEEWVCDEDSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TFSKN----VMMIQSCKCNYNCPHANEAAFPFYRLFNDIHKFRD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GCGCCKVCAKQLNEDCSKTQPCDHTKGLECNFGASSTALKGICRAQSEGRPCEYNSRIYQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TKKSPEPVRFTYAGCLSVKKYRPKYCGSCVDGRCCTPQLTRTVKMRFRCED------GE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TKKSPEPVRFTYAGCLSVKKYRPKYCGSCVDGRCCTPQLTRT-----CEDAVPLRRWGD
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                                  Conservative
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                                                                                                     AA;
                                                                                                                   CTCK_1; 1.
CTCK_2; 1.
TSP1; 1.
VWFC; 1.
                                                  44.3%;
                                                                                                     37966 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       75.0%;
                                  51;
                               Score 938; DB
Pred. No. 5.8e
51; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5
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Pred.
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No. 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Vertebrata;
                               DB 13;
5.8e-83;
nes 95;
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1.8e-146;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A
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                                                                                                                                                                                                                                                                                                                                                                                                                                          databases
                                                                                                   CRC64;
                                                              Length 343;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length
                                  Indels
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                                 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22;
                                 Gaps
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Query Match
Best Local
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CPAACHCPLEAPKCAPGVGLVRDGCGCCKVCAKQLNEDCSKTQPCDHTKGLECNFGASST

85

Similarity

DB 13; .5e-82;

Length

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                                                                                                                                                                                  Pfam; PF00007; Cys_knot; 1
Pfam; PF000219; IGFBP; 1.
Pfam; PF00090; tsp_1; 1.
Pfam; PF00093; vwc; 1.
SMART; SM00041; CT; 1.
SMART; SM00121; IB; 1.
SMART; SM00121; IB; 1.
SMART; SM00214; VWC; 1.
PROSITE; PS01185; CTCK_1;
                                                 CHAIN
SEQUENCE
                                                                                   Signal.
                                                                                                                 PROSITE;
PROSITE;
PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                             Mukudai Y., Kubota S., Takig
Submitted (DEC-2001) to the
EMBL; AJ298335; CAC33438.1;
EMBL; AF463517; AAL68834.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gygi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
Connective tissue growth factor precursor (Connective factor/hypertrophic chondrocyte-specific protein 24).
Gallus gallus (Chicken).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                       PROSITE;
                                                                                                                                                                                                                                                                                                                                              InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (JAN-2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9031;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q98TQ8
                                                                                                                                                                                                                                                                                                                                                           InterPro;
                                                                                                                                                                                                                                                                                                                                                                              InterPro;
                                                                                                                                                                                                                                                                                                                                                                                              InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                              InterPro;
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                                                                                                                                     ; PS01225; CTCK_1; 1.
; PS01225; CTCK_2; 1.
; PS00222; IGF PT***
                                                                                                                     PS50092;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTPQLTRTVKMRFRCEDGETFSKNVMMIQSCKCNYNCPHANE--AAFPFYRLFNDI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RKIGVCTAR-EGAPCVFGGTVYRSGESFQSSCKYQCTCIDGGVGCVPLCSMDIRLPSPEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ALKGICRAQSEGRPCEYNSRIYQNGESFQPNCQHQCTCIDGAVGCIPLCPQELSLPNLGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTPHRTATLPVEFKCPDGEVMKKNMMFIKTCACHFNCPGDNDIFEAMYYRKMYGDM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QSRLCMVRPCEADLEENIKKGKKCIRTPKISKPVKFEFSGCTSVKTYRAKFCGVCTDGRC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ETRICEVRPCGQPVYSSLKKGKKCSKTKKSPEPVRFTYAGCLSVKKYRPKYCGSCVDGRC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----LPAFRMEE--TYGPDPSLIRANCLVQTTEWSACSKTCGMGISTRVTNDNEHCRLEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SLKRLPVFGMEPRILYNP----LQGQKCIVQTTSWSQCSKTCGTGISTRVTNDNPECRLVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PFPRRVKLPGKCCEEWVCDQP----------------------------------QERTLVGPA-
                                                                                                                                                                                                                                                                                                                                                    IPRO06208; Cys_knot.
IPRO06207; Cys_knot_C.
IPRO06867; Insl_gro_fac_pr.
IPRO00864; TSP1.
                                                                                                                                                                                                                                                                                                                                             IPR001007; VWF_C.
                                                   344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N.A.
                                                   AA;
                                                                                                              IGF_BINDING;
; TSP1; 1.
; VWFC; 1.
                                                 344
37499
44.0%;
45.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the EMBL/GenBank/DDBJ
                                                   WW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL/GenBank/DDBJ
                                              POTENTIAL.
CONNECTIVE TISSUE 0
59E639AF69BF1D00
Score 930;
Pred. No. 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    X
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                                                                 TISSUE GROWTH FACTOR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  databases
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                                                   CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAY-2000
01-MAY-2000
01-MAR-2003
                     SMART;
                                                  SMART;
                                                                                                                                                                           InterPro;
InterPro;
                                                                                Pfam;
                                                                                               Pfam;
                                                                                                                                                                                                                                    retinoid regulation in limb
Gene 222:119-124(1998).
                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. TISSUE=Forelimb bl
                                                                                                                                                                                                                                                                                                                                                                                    [1]
SEQUENCE FROM N.A.
Sequence from blastema;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Notophthalmus viridescens (Eas
Eukaryota; Metazoa; Chordata;
Amphibia; Batrachia; Caudata;
                                                                                                                                                                                                                        EMBL; AJ271167; CAB65965.1; -.
                                                                                                                                                                                                                                                                                        Cash D.
                                                                                                                                                                                                                                                                                                   MEDLINE-99033008;
                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Forelimb
Gates P.B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9PT80;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9PT80
                                                                                                                                                InterPro;
                                                                                                                                                              InterPro;
                                                                                                                                                                                                        InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Notophthalmus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Connective
                                                                                                                                                                                                                                                    MEDIINE-99033008; PubMed-9813273;
Cash D.E., Gates P.B., Imokawa Y., Brockes J.P.;
"Identification of newt connective tissue growth
retinoid regulation in limb blastenal cells.";
                PF00007; Cys_knot; :
PF00020; IGFBP; 1.
PF00090; tsp_1; 1.
PF00093; vwc; 1.
; SM00041; CT; 1.
; SM00121; IB; 1.
; SM00214; VWC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          271
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AVGCIPLCPQELSLPNLGCPNPRLVKVTGQCCEEWVCDEDSIKDPMEDQDGLLGKELGFD
                                                                                                                                                      IPR006208; Cys_knot.
IPR006207; Cys_knot_C.
IPR000867; Insl_gro_fac_pr.
IPR000884; TSP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AFPFY - - RLFNDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VKTYRAKECGVCTDGRCCTPHRTATLPVEFKCPDGEIMKRKMMFIKTCACHYNCPGDNDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VKKYRPKYCGSCVDGRCCTPQLTRTVKMRFRCEDGETFSKNVMMIQSCKCNYNCPHANEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GISTRYTNDNAFCRIEKQSRICMVRPCEADLEENIKKGKKCIRTPKISKPIKFELSGCTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GISTRVTNDNPECRLVKETRICEVRPCGQPVYSSLKKGKKCSKTKKSPEPVRETYAGCLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ASEVELTRNNELIAVGKGRSLKRL-PVFGMEPRILYNPLQGQKCIVQTTSWSQCSKTCGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AVGCVPLCSMDVRLPSPDCPYPRRVKLPGKCCEEWVCDE-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FESLYYRKMYGDM
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                                                                                                                                              IPR001007;
                                                                                                                                                                                                                                                                                                                                                               (JAN-2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    O (TrEMBLrel. 13, Created)
O (TrEMBLrel. 13, Last sequence update)
3 (TrEMBLrel. 23, Last annotation update)
tissue growth factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                   blastema;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -AKEQTAVGPALAAYRLEDTYGPDPTMM
                                                                                                                              VWF_C.
not; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (Eastern newt) (Triturus viridescens).
ata; Craniata; Vertebrata; Euteleostomi;
ata; Salamandroidea; Salamandridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   59;
                                                                                                                                                                                                                                                                                                                                                               EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  347
                                                                                                                                                                                                                                                      ssue growth cells.";
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Best Local
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01-MAY-1999
01-MAR-2003
                                                                                                          InterPro;
Pfam; PF00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE;
PROSITE;
PROSITE;
PROSITE;
SEQUENCE
 SMART;
                                                                                                                                                        InterPro;
InterPro;
                                                                             Pfam;
                                                                                                                                                                                                                                                                                                                                             Sus scrofa (Pig).
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                  SMART;
                                              SMART;
                                                                                             Pfam;
                                                                                                                                         InterPro;
                                                                                                                                                                                      InterPro;
                                                                                                                                                                                                        EMBL;
                                                                                                                                                                                                                     Submitted
                                                                                                                                                                                                                                                                    Harding P.A.,
                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                              CTGF
                                                                                                                                                                                                                                                                                                                                                                                                            Connective tissue
                                                                                                                                                                                                                                    (CTGF) cDNA. "
                                                                                                                                                                                                                                                  "Cloning and sequencing
PF00093; V
F; SM00041;
SM00121;
SM00209;
SM00214; V
                                                                            PF00007;
PF00219;
PF00090;
                                                                                                                                                                                                       tted (SEP-1996) to the U70060; AAD00174.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   337
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;; PS01225; CTCK_2; 1.
;; PS00222; IGF_BINDING; 1
;; PS50092; TSP1; 1.
;; PS01208; VWFC; 1.
;; PS01208; VWFC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YRPKYCGSCVDGRCCTPQLTRTVKMRFRCEDGETFSKNVMMIQSCKCNYNCPHANEAAFP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TRVINDNEMCRLEKQSRLCMVRPCEADLEENIKKGKKCIRTPKISKPVKFELSGCTSVKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TRVTNDNPECRLVKETRICEVRPCGQPYYSSLKKGKKCSKTKKSPEPVRFTYAGCLSVKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EVELTRNNELIAVGKGRSLKRLPVFGMEPRILYNPLQGQKCIVQTTSWSQCSKTCGTGIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VCDPHRGLFCDEGSRVNKKIGVCTAK-DGAPCVFGGMYYRSGESFQSSCKYQCTCLDGGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PCDHTKGLECNFGASSTALKGICRAQSEGRPCEYNSRIYQNGESFQPNCQHQCTCIDGAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LALVVTLLHLTRLALSTCPAACHCPLEAPKCAPGVGLVRDGCGCCKVCAKQLNEDCSKTQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MYYRKMYGDM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FY--RLFNDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YRAKFCGVCTDGRCCTPHRTATLPVEFKCPDGEVMKKKMMFIKTCACHYNCPGDNDIFES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      --EQTRVGPALAV----YRQEETYGPD----SSLMRANCLVQTTEWSACSKTCGMGIS
                                                                                                          IPR001007; VWF
0007; Cys_knot;
                                                                                                                                      IPR006208; Cys_knot.
IPR006207; Cys_knot_C.
IPR000867; Insl_gro_fac_pr.
IPR000884; Tsp1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LLLAVALLSWVSCA-QDCSGECRCPNKPPECPAGTSLVMDGCGCCKVCAKQLGELCTEKD
                                                                                                                                                                                                                                                                                                                                                                                                         (TrEMBLrel. 10, Created)
(TrEMBLrel. 10, Last sequence up
(TrEMBLrel. 23, Last annotation
tissue growth factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                tsp_1;
vwc; 1.;
cT; 1.
l; CT; 1.
                                                                                                                                                                                                                                                                   Brigstock
                                                                                            IGFBP;
 TSP1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                376
                                                                                                                                                                                                                                                                                                                                             Chordata; Craniata; Vertebrata; Cetartiodactyla; Suina; Suidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 346
                                                                                                            VWF_C.
not; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      43.1%;
45.1%;
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R.;
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                                                                                                                                                                                                                     EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score .912.5; DB 13; Pred. No. 1.8e-80; 4; Mismatches 112;
                                                                                                                                                                                                                                                    porcine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
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                                                                                                                                                                                                                                                    connective tissue
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Sus.
                                                                                                                                                                                                                                                    growth
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Best Local
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OBCA67:
01-MAR-2003 (TrEMBLrel. 23, Last seq
01-MAR-2003 (TrEMBLrel. 23, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE;
PROSITE;
PROSITE;
PROSITE;
                                                                                                  the RIKEN Genome Exploration Research Group "Analysis of the mouse transcriptome based c 60,770 full-length cDNAs.";
Nature 420:563-573(2002).
EMBL; AK039481; BAC30363.1; -.
                                                                                                                                                                                                     Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                           SEQUENCE
                                                                                                                                                  The
                                                                                                                                                          STRAIN=C57BL/6J; TISSUE=Spinal cord; MEDLINE=22354683; PubMed=12466851;
                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                              NCBI_TaxID=10090;
                                                                                                                                                                                                                                 Nephroblastoma overexpressed.
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                                                                Similarity
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PS50092;
PS01208;
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PS01225;
                              RALALVVTLLH-LTRLALS-TCPAAC--HCPLEAPKCAPGVGLVRDGCGCCKVCAKQLNE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QPCDHTKGLECNFGASSTALKGICRAQSEGRPCEYNSRIYQNGESFQPNCQHQCTCIDGA
DCSKTQPCDHTKGLECNFGASSTALKGICRAQSEGRPCEYNSRIYQNGESFQPNCQHQCT 122
                                                                                                                                                                                                                                                                                                                                              FPFY--RLFNDI 376
                                                                                                                                                                                                                                                                                                                                                                          KKYRPKYCGSCVDGRCCTPQLTRTVKMRFRCEDGETFSKNVMMIQSCKCNYNCPHANEAA
                                                                                                                                                                                                                                                                                                                                                                                                             ISTRYTNDNPECRLVKETRICEVRPCGQPVYSSLKKGKKCSKTKKSPEPVRFTYAGCLSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VGCVPLCSMDVRLPSPDCPFPRRVKLPGKCCEEWVCDEP--------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VGCIPLCPQELSLPNLGCPNPRLVKVTGQCCEEWVCDEDSIKDPMEDQDGLLGKELGFDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APCDPHKGLFCDFGSPANRKIGVCTAK-DCAPCVFGGTVYRSGESFQSSCKYQCTCLDGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ALVVTLLHLTRLAL-STCPAACHCPL-EAPKCAPGVGLVRDGCGCCKVCAKQLNEDCSKT 67
                  RCLCLGFLLFHLLSQVSASLRCPSRCPPKCPSISPTCAPGVRSVLDGCSCCPVCARQRGE
                                                                                                                                                                                                                                                                                                                             ESLYYRKMYGDM
                                                                                                                                                                                                                                                                                                                                                                 KTYRAKFCGVCTDGRCCTPHRTTTLPVEFKCPDGEVMKKSMMFIKTCACHYNCPGDNDIF 336
                                                                                                                                                                                                                                                                                                                                                                                                   ISTRVTNDNASCRLEKQSRLCMVRPCEADLEENIKKGKKCIRTPKISKPVKFELSGCTSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEVELTRNNELIAVGKGRSLKRL-PVFGMEPRILYNPLQGQKCIVQTTSWSQCSKTCGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AFVLLLALCSRPASGQDCSGQCQCAAGKRRACPAGVSSLLEGCGCCRLCAKHLGDLCTER
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                                                       Conservative
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CTCK_2; 1.
; CTCK_2; 1.
; IGF_BINDING;
; TSP1; 1.
; VWFC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                        -KDHTVVGPALAAYRLEDTFGPDPTMM-----RANCLVQTTEWSACSKTCGMG
                                                                                           38828 MW;
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                                                               38.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 41.5%;
                                                                                                                                                                                                                                                                                                                            348
                                                       46;
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                                                    Score 822; DB 11;
Pred. No. 1.2e-71;
46; Mismatches 120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 878;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. 4.1e-77;
                                                                                                                                                                                                      Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                           6F3B34A3A84187EE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            35AB4275AC1D4B3A CRC64;
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on functional
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                                                      Indels
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                                                      36;
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                 67
                                   62
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PROSITE;
                 SMART;
                                                     Pfam;
                                                                                                  InterPro;
InterPro;
                                   SMART;
                                                                                                                                                                 Submitted
                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                      095388
                                             SMART;
                                                                Pfam;
                                                                         Pfam;
                                                                                Pfam;
                                                                                           InterPro;
                                                                                                                     InterPro;
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                                                                                                                                                 EMBL;
                                                                                                                                                          EMBL;
                                                                                                                                                                            Rosenthal
                                                                                                                                                                                    Jonge R.d.,
                                                                                                                                                                                            Blechschmidt
                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                               095388
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                         n; PF00090; tsp_1;
n; PF00093; vwc; 1.
XT; SM00041; CT; 1.
XT; SM00121; IB; 1.
XT; SM00209; TSP1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             337
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                  SM002
PS01185; CTCK_1;
PS01225; CTCK_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NNEA 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ANEA 365
                                                                                           IPR001007;
                                                                                                             IPR000867;
                                                                                                                                                                                   Schilhabel
                  VWC;
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Pennica D., Swanson T.A., Welsh J.W., Roy M.A., Lawrence I Brush J., Taneyhill L.A., Deuel B., Lew M., Watanabe C., C Melham M.F., Finley G.G., Quirke P., Goddard A.D., Hillan Gurney A.L., Botstein D., Levine A.J.; "MISP genes are members of the connective tissue growth fa "MISP genes are members of the connective cells and aberr expressed in human colon tumors."; proc. Natl. Acad. Sci. U.S.A. 95:14717-14722(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAY-1999 (TrEMBLrel. 10,
01-MAY-1999 (TrEMBLrel. 10,
01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Lung, and Fetal kidney;
MEDLINE=99061933; PubMed=9843955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Connective tissue growth
PF00007; Cys_knot; 1.
PF00219; IGFBP; 1.
PF00090; tsp_1; 1.
                                                                                                                                                                                          AF100779; AAC96321.1; -. AF192304; AAF22341.1; -.
                                                                                                                                                                           HGNC:12769; WISP1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GCLSVKKYRFKYCGSCVDGRCCTPQLTRTVKMRFRCEDGETFSKNVMMIQSCKCNYNCPH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CGTGISTRVTNDNPECRLVKETRICEVRPCGQ-PVYSSLKKGKKCSKTKKSPEPVRFTYA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CRDGQIGCLPRCQLDVLLPGPDCPAPRKVAVPGECCEKWTCGSDE-----QGTQGTLG-G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CIDGAVGCIPLCPQELSLPNLGCPNPRLVKVTGQCCEEWVCDEDSIKDPMEDQDGLLGKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCTSLYTYKPRFCGVCSDGRCCTPHNTKTIQVEFQCLPGEIIKKPVMVIGTCTCYSNCPQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CGMGVSTRVINRNRQCEMVKQTRLCIVRPCEQEPEEVTDKKGKKCLRTKKSLKAIHLQFE
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                                                                                                                            IPR006208; Cys_knot.
IPR006207; Cys_knot_C
                                                                                                                                                                                                                                    (OCT-1999) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                               Kalaydjieva L., Good
Lhabel M., Schattevoy
                                                                VWF_C
                                                                                        TSP1
                                                                                                        Insl_gro_fac_pr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Craniata; Vertebrata; | Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                 Goodman R., Gresham D.,
tevoy R., Dette M., Menze
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    367
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Cohen
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                                                                                                                                                                                                                                                                                                                                                                                                                                      family
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rattus norvegicus (Rattus norvegicus);
Eukaryota; Metazoa; (
Mamumalia; Eutheria; )
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-2001
01-JUN-2001
01-MAR-2003
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PROSITE;
SEQUENCE
                 SMART;
SMART;
SMART;
                                                                                                    Pfam;
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Pfam;
                                                                                                                                                                Pfam;
                                                                                                                                                                                                       EMBL; AF228049; AAK00729.1; -.
InterPro; IPR006208; Cys_knot_C.
InterPro; IPR006207; Cys_knot_C.
InterPro; IPR000867; Insl_gro_fe
InterPro; IPR000884; TSP1.
                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE-20487548; PubMed-11031104;
Sleeman M.A., Murison J.G., Strach
Sleeman M.A., Murison J.G., Griere
                                                                                   SMART;
                                                                                                                                                                                                                                                                                                                Genomics
                                                                                                                                                                                                                                                                                                                                                                            Sleeman M.A., Murison J.G., McGrath A., Bickerstaff P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ELM1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q99PPO;
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                                                                                                                                                                                          InterPro;
                                                                                                                                                                                                                                                                                                                                                          Watson
                                                                                                                                                                                                                                                                                                              "Gene expression in rat dermal Genomics 69:214-224(2000).
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1; PF0007; Cys.knot; 1.
1; PF00219; IGFBP; 1.
1; PF00099; tsp. 1; 1.
1; PF00099; vwc; 1.
1; SM00041; CT; 1.
1; SM00121; IB; 1.
2; SM00121; IB; 1.
3; SM00121; VwC; 1.
5; PS01195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          340
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148; Conserv
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                                                                                                                                                                                                                                                                                                                                                          J.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PS50092; TSP1; 1.
PS01208; VWFC; 1.
367 AA; 40331
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oa; Chordata;
ia; Rodentia;
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38.0%;
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                                                                                                                                                                                                                                                                                                                                                                            Strachan
Grierson
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Last sequence update)
Last annotation updat
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Pred. No. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Craniata; Vertebrata; | Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                    papilla
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                                                                                                                                                                                                                                                                                                                                    ESTs.";
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                                                                                                                         MEDLINE-98119879; PubMed=2449709; Hashimoto Y., Shindo-okada N., Tani M., Nagamachi Y., Takeuchi K., Shiroishi T., Toma H., Yokota J.; Shiroishi T., Toma H., Yokota J.; Expression of the Elml gene, a novel gene of the CCN (connective tissue growth factor, Cyr61/Cef10, and neuroblastoma overexpressed gene) family, suppresses In vivo tumor growth and metastasis of K-1 murine melanoma cells.";
                                                                                                                                                                                                                                                                                                           01-JUN-1998
01-JUN-1998
01-MAR-2003
                                                                                                          J. Exp. Med. [2]
                                                                                                                                                                                                                                                                                                                                               054775
054775;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE;
PROSITE;
PROSITE;
SEQUENCE
                             TISSUE-Mammary gland;
MEDLINE-99061933; PubMed-9843955;
Pennica D., Swanson T.A., Welsh J.W., Ro
Brush J., Taneyhill L.A., Deuel B., Lew
Melham M.F., Finley G.G., Quirke P., God
Gurney A.L., Botstein D., Levine A.J.;
          "WISP genes are members of the connective that are up-regulated in wnt-1-transformed
                                                                                                                                                                                                                                                       Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                           NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                             Mus musculus
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149; Conser
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PS50092;
PS01208;
367 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QQLGDNCTEAAVCDPHRGLYCDYSGDRPRYAIGVC-AQVVGVGCVLDGVRYTNGESFQPN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATNFTLAGCVSTRTYRPKYCGVCTDNRCCIPYKSKTISVDFQCPEGPGFSRQVLWINACF
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                                                                                                                                                                                                                                                                                                             (TrEMBLrel.
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 human
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                                                                                                                                                                                                                                                                             (Mouse)
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TSP1; 1
VWFC; 1
 colon
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Rodentia;
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38.5%;
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          wnt-1-transformed
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Last
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                                                                                                                                                                                                                                                                                                                                  Created)
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2; Mismatches
                                                                                                                                                                                                                                                       Craniata; Vertebrata;
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                           PRT;
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                                          Goddard
                                                      Roy M.A.,
ew M., Wat
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.1e-65;
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                      tissue
           cells
                                         f.A., Lawrence D
  Watanabe C., C
d A.D., Hillan
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           and aberrantly
                    growth factor family
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; Murinae; Mus
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                                                     D.A.,
Cohen
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                                                      Lee J
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LIBC,

Root H.,
S.D.; and

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Best Local S
Matches 149
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Pfam; PF00007; Cys knot; 1.

Pfam; PF000219; IGFBP; 1.

Pfam; PF00090; tsp_1; 1.

Pfam; PF00090; tsp_1; 1.

SMART; SM00041; CT; 1.

SMART; SM000209; TSP1; 1.

SMART; SM00214; VWC; 1.

SMART; SM00214; VWC; 1.

PROSITE; PS01125; CTCK_2; 1.

PROSITE; PS01092; TSP1; 1.

PROSITE; PS01092; TSP1; 1.

PROSITE; PS01092; TSP1; 1.

PROSITE; PS01092; TSP1; 1.

SEQUENCE 367 AA; 40702 MW; 3
                                                                                       (Fragment).
DJ142L7.3 (
                                      Fragme...

D714217.3 OR LILE.

Homo sapiens (Human).

Homo sapiens (Human).

Horvota; Metazoa; Chordata; Metazoa; Primates;
                                                                                                                         095958;
01-MAY-1999 (TrEMBLrel.
01-MAY-1999 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Proc.
EMBL;
EMBL;
MGD; 1
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InterPro; IPR006207; Cys_knot_C.
InterPro; IPR000867; Insl_gro_fac_pr.
InterPro; IPR000884; TSP1.
              SEQUENCE FROM
                                                                                                                 DJ142L7.3
                                                                                                                                                                               095958
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      al Similarity
149; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                CQHQCTCIDGAVGCIPLC--PQELSLPNLGCPNPRLVKVTGQCCEEWVCDEDSIKDPMED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LATALSPTPTTMTFTPAPLEETTTRPEFCKWPCECPQSPPRCPLGVSLITDGCECCKICA
                                                                                                                                                                                                                                           CNLSCRNPND-----
                                                                                                                                                                                                                                                                                                        PVRFTYAGCLSVKKYRPKYCGSCVDGRCCTPQLTRTVKMRFRCEDGETFSKNVMMIQSCK
                                                                                                                                                                                                                                                                                                                                                           SWSQCSKTCGTGISTRYTNDNPECRLVKETRICEVRPCGQPVYSSLKKGKKCSKTKKSPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IARALALVVTLLHLTRLALST------CPAACHCPLEAPKCAPGVGLVRDGCGCCKVCA
                                                                                                                                                                                                                                                                   CNYNCPHANEAAFPFYRLFNDIHKFRD 381
                                                                                                                                                                                                                                                                                            ATNETLAGCVSTRTYRPKYCGVCTDNRCCIPYKSKTISVDFQCPEGPGFSRQVLWINACF
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                                                                                                                                                                                                                                                                                                                                                                                              QTALLDTRAFAASGAVEQRYEN--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KQLNEDCSKTQPCDHTKGLECNF-GASSTALKGICRAQSEGRPCEYNSRIYQNGESFQPN
                                                                                                               (Connective tissue
                                                                                                                                                                              PRELIMINARY;
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              N.A
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23,
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                                                                                                                            Last sequence update)
Last annotation updat
                                                                                                                                                      Created)
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Pred. No. 2.1e
52; Mismatches
                                                                                                               growth
                                                Craniata; Vertebrata; Catarrhini; Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           95:14717-14722(1998).
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                                                                                                             factor (NOV, GIG) like protein)
                                                                                                                                                                                                                                           361
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2.1e-65;
                                                                                                                                                                              Ä
                                                  Hominidae;
                                                                                                                             update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 367;
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                                                               Euteleostomi;
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RESULT 13
09538
ID 09538
AC 09538
AC 09538
AC 01-MA
DT 01-MA
DT 01-MA
DT Conne
GN WISPS
GOS Homo
OC Eukaa
OX Mamma
OX NCBI_
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RP SEQUE
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Best Local
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Pfam; PF00219; IGFBP; 1.
Pfam; PF00090; tsp_1; 1.
SMART; SM00041; CT; 1.
SMART; SM00121; IB; 1.
SMART; SM00209; TSP1; 1.
PROSITE; PS01222; IGF_BINDING
PROSITE; PS00222; IGF_BINDING
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PROSITE;
PROSITE;
NON_TER
SEQUENCE
                                                                                                 01-MAY-1999 (TrEMBLrel. 10, Crea 01-MAY-1999 (TrEMBLrel. 10, Last 01-MAR-2003 (TrEMBLrel. 3, Last Connective tissue growth factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (APR-1999) to the EMBL; Z99289; CAB16556.1; -. EMBL; AF143679; AAD31517.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 van Golen K.L., Davies S., Wu Z.F., Wang Y.F., Bucana C.D., Chandrasekharappa S., Strawderman M., Ethier S.P., Merajver "A novel putative IGF-binding, tumor suppressor protein, LIF RhoC GTPase, are determinants of the inflammatory breast car
                                                Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                 095389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    phenotype."
             SEQUENCE FROM N.A.
                          NCBI_TaxID=9606;
                                                                           Homo sapiens (Human)
                                                                                        WISP3
                                                                                                                                                     095389;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Mammary gland;
van Golen K.L., Davies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (MAR-1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro;
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[SSUE=Bone marrow,
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                                                                                                                                                                                                                              CIPNKSKMITIQFDCPNEGSFKWKMLWITSCVCQRNC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PS50092;
                                                                                                                                                                                                                                                                                               RICEVRPCGQPYYSSLK--KGKKCSKTKKSPEPVRFTYAGCLSVKKYRPKYCGSCVDGRC
                                                                                                                                                                                                                                                                                                                              TSYKTMPAYRNLPLI-----WKKKCLVQATKWTPCSRTCGMGISNRVTNENSNCEMRKEK
                                                                                                                                                                                                                                                                                                                                             RSLKRLFVFGMEPRILYNPLQGQKCIVQTTSWSQCSKTCGTGISTRVTNDNPECRLVKET
                                                                                                                                                                                                                                                                                                                                                                                 ----IPKLAGSHC---
                                                                                                                                                                                                                                                                                                                                                                                                                                                 ALK-GICRAQSEGRPCEYNSRIYQNGESFQPNCQHQCTCIDGAVGCIPLCPQELSLPNLG
: |:| :| | | |:| | ||: |||| | |: ||:|| ||
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CPAACHCPLEAPKCAPGVGLVRDGCGCCKVCAKQLNEDCSKTQPCDHTKGLECNFGASST
                                                                                                                                                                                                                                                      CTPQLTRTVKMRFRCEDGETFSKNVMMIQSCKCNYNC
                                                                                                                                                                                                                                                                                                                                                                                                           CPNPRLVKVTGQCCEEWVCDEDSIKDPMEDQDGLLGKELGFDASEVELTRNNELIAVGKG
                                                                                                                                                                                                                                                                                                                                                                                                                                  RYETGYCACKSYG--CEFNQVHYHNGQVFQPNPLFSCLCVSGAIGCTPLF------
                                                                                                                                                                                                                                                                               RLCYIQPCDSNILKTIKIPKGKTCQPTFQLSKAEKEVFSGCSSTQSYKPTFCGTCLDKRC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IPR006208; Cys_knot.
IPR006207; Cys_knot_C.
IPR000867; Insl_gro_fac_pr.
IPR000884; TSP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        331 AA;
                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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                                                Chordata;
Primates;
 and
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Fetal kidney;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      50;
                                                                                               Last sequence update)
Last annotation update)
ctor related protein WISP-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 626.5;
Pred. No. 1.2e
50; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL/GenBank/DDBJ
                                                                                                                                        Created)
                                                Craniata; V
Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        D109C2FDCA1DF549 CRC64;
                                                                                                                                                                 354
                                                               Vertebrata;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   . 2e-52;
                                                                                                                                                                 A
                                                  Hominidae;
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Indels

47;

Gaps

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85 8;

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Best Local
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Pfam; PF000219; IGBBP; 1.
Pfam; PF00090; tsp_1; 1.
SMART; SM00041; CT; 1.
SMART; SM00021; IB; 1.
SMART; SM00121; IB; 1.
SMART; SM00209; TSP1; 1.
PROSITE; PS001225; CTCK_2; 1.
PROSITE; PS001225; IGF_BINDING; 1
PROSITE; PS00222; TSP1; 1.
                                                                                                                                                                                                                                                                                                                                                                             Q8CIC8;
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"WISP genes are members of the connective tissue growth factor family that are up-regulated in wnt-1-transformed cells and aberrantly expressed in human colon tumors.";

Proc. Natl. Acad. Sci. U.S.A. 95:14717-14722(1998).
                                                         SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Mammary gland;
                                                                                                                                                                                   Mus musculus (Mouse).
Eukaryota; Metazoa; C
Mammalia; Eutheria; F
                                                                                                                                                                                                                                               01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Similar to WNT1 inducible signaling pathway protein
                             Submitted
                                                   Strausberg R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AF100781; AAC96323.1; -. Genew; HGNC:12771; WISP3.
                                                                                                                                                        NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR006208; Cys_knot.
InterPro; IPR0068207; Cys_knot_C.
InterPro; IPR000867; Insl_gro_fac_pr.
InterPro; IPR000884; TSP1.
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BC032877;
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21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RICEVRPCGOPVYSSLK--KGKKCSKTKKSPEPVRETYAGCLSVKKYRPKYCGSCVDGRC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TSYKTMPAYRNLPLI-----WKKKCLVQATKWTPCSRTCGMGISNRVTNENSNCEMRKEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RSLKRLPVFGMEPRILYNPLQGQKCIVQTTSWSQCSKTCGTGISTRVTNDNPECRLVKET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CPNPRLVKVTGQCCEEWVCDEDSIKDPMEDQDGLLGKELGFDASEVELTRNNELIAVGKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RYETGVC-AYLVAVGCEFNQVHYHNGQVFQPNPLFSCLCVSGAIGCTPLF------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CHWPCKCPQQKPRCPPGVSLVRDGCGCCKICAKQPGEICNEADLCDPHKGLYCDYSVDRP
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                        (JUN-2002)
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AAH32877.1;
                                                                                                                                                                                   Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29.0%;
35.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      49;
                   EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 613; DB 4;
Pred. No. 2.6e-51;
                                                                                                                                                                              Craniata; Ver
Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                   251
                                                                                                                                                                                                         Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121;
                                                                                                                                                                                   Muridae;
                           databases
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                                                                                                                                                                                                            Euteleostomi;
                                                                                                                                                                                                                                                                   2
                                                                                                                                                                                   Murinae;
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1 R.L.,
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tanaka S., Sugimachi K.;
"Human WISP-1 variant.";
Submitted (NOV-1999) to the EMBL/GenBar
EMBL; AB034725; BAB17849.1; -
InterPro; IPR006208; Cys_knot_C.
InterPro; IPR006307; Cys_knot_C.
InterPro; IPR00867; Insl_gro_fac_pr.
                                                                                                                                                                                                                                                                                                                 Pfam; PF00219; IGFBP; 1.
Pfam; PF00090; tsp_1; 1.
SMART; SM00041; CT; 1.
SMART; SM00121; IB; 1.
SMART; SM001209; TSP1; 1.
PR0SITE; PS01185; CTCK_1; 1
PR0SITE; PS01225; CTCK_2; 1
PR0SITE; PS01225; CTCK_2; 1
PR0SITE; PS01225; TSP1; 1.
SEQUENCE 280 AA; 30697 M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAR-2001
01-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR000884; TSP:
Pfam; PF00007; Cys_knot;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human)
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                                                                                    55 VCAKQLNEDCSKTQPCDHTKGLECNFGASSTALKGICRAQSEGRPCEYNSRIYQNGESFQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64
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99; Conserv
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PNCQHQCTCIDGAVGCIPLCPQELSLPNLGCPNPRLVKVTGQCCEEWVCDEDSIKDPMED
                                            MCAQQLGDNCTEAAICDPHRGLYCDY-
                                                                                                                                  STVLATALSPAPTTMDFTPAPLEDTSSRPQFCKWPCECPPSPPRCPLGVSLITDGCECCK
                                                                                                                                                                            SSRIARALALVVTLLHLTRLALST-----CPAACHCPLEAPKCAPGVGLVRDGCGCCK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LLHLTRLALS-----TCPAACHCPLEAPKCAPGVGLVRDGCGCCKVCAKQLNED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CDHLHVCNPSQGLVCQPGAGPSGRGVVCLFEEDDGSCEVNGRRYLDGETFKPNCRVLCRC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LIHL--LAISFLCILSMVYAQLCPAPCACPWTPPQCPPGVPLVLDGCGCCRVCARRLGES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IPR000884; TSP1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        251
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                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chordata;
Primates;
                                                                                                                                                                                                                                                  23.4%; 27.9%;
                                                                                                                                                                                                                                                                                                                      30697 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27106 MW;
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16,
23,
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, Last sequence up
, Last annotation
                                                                                                                                                                                                                             49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               36; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                Score 495.5;
Pred. No. 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 514.5; DB 1
Pred. No. 6.8e-42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Craniata; Vertebrata; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        57520309A9069524 CRC64;
                                                                                                                                                                                                                                                                                                                    26B254D4A060738E CRC64;
                                                                                                                                                                                                                             Mismatches
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                                                                                                                                                                                                                                                  4e-40;
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                                                                                                                                                                                                                                                                       DB 4;
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                                                                                                                                                                                                                             137;
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                                            RYAIGV---
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Searc	DЬ	Qy	Db	Qy	Db	Qy	Db	Qy	Db
Search completed: Augus Job time : 34.0868 secs	255 (355 (195	295 1	135 1	235 (121	175 (115 -
Search completed: August 5, 2003, 14:06:51 Job time : 34.0868 secs	255 CNLSCRNPNDIFADLESYPD 274	PFY	195 SMNFTLAGCISTRSYQPKYCGVCMDNRCCIPYKSKTIDVSFQCPDGLGFSRQVLWINACF 254	295 PVRFTYAGCLSVKKYRPKYCGSCVDGRCCTPQLTRTVKMRFRCEDGETFSKNVMMIQSCK 354	135 PWSPCSTSCGLGVSTRISNVNAQCWPEQESRLCNLRPCDVDIHTLIKAGKKCLAVYQPEA. 194	235 SWSQCSKTCGTGISTRYTNDNPECRLVKETRICEVRPCGQPYYSSLKKGKKCSKTKKSPE 294	EVEAWHRN	NELIAVGKGRSLKRLPVFGMEPRILYNPLQGQK	115CAHAVG
			ČF -	- ČK	ĔA. 1	PE 2	SIS	T	
			254	354	.94	294	134	234	120

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